us-10-724-972a-6352.rai

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2005, 09:19:57; Search time 23 Seconds (without alignments) 1087.280 Million cell updates/sec Run on:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL......EEMAKELVELSKKDSKKDNK 335 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched: 513545 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 16, Appl Sequence 5193, Ap Sequence 5193, Ap	16, 4516 5492	6862, 462, A 1268, 38, Ap	Sequence 4342, Ap Sequence 5565, Ap Sequence 40, Appl Sequence 572, Appl Sequence 4860, Ap	29723 29723 29723 2001 2001 1001
SOUTHERES	US-09-830-217-16 US-08-956-171E-5193 US-08-781-986A-5193	946-16 532A-45 001C-54	09-543-681A-6 09-710-279-46 09-710-279-12 09-071-035-38	US-09-134-000C-4342 US-09-543-681A-5565 US-09-071-035-40 US-09-602-787A.572 US-09-134-001C-4860	US-09-583-110-3723 US-09-583-110-3723 US-09-107-433-4809 US-09-017-78-598 US-09-071-035-70 US-09-071-035-70 US-08-516-08-24 US-09-536-784-24 US-09-134-00C-6014 US-09-071-035-72 US-09-071-035-72 US-09-302-6268-10
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% Query Match Length DB	330	330 352 351	351 347 347 317	325 325 296 306 60	335 325 325 332 332 321 321 321 321
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Score	405 405 405	405 307.5 296.5	292 292 293 293	283 278.5 268 266 266	255 250 250 250 250 250 250 250 236 236 236 236 236 236 236
Result No.	404	1 4 N O	7 8 10	11 13 14 15	2010 2010 2010 2010 2010 2010 2010 2010

Sequence 4519, Ap Sequence 1888, Ap Sequence 5667, Ap Sequence 9745, Ap Sequence 1159, App Sequence 1159, App Sequence 12270, Ap Sequence 7224, App Sequence 12270, App Sequence 194, App Sequence 194, App Sequence 1, Appli Sequence 6, Appli Sequence 6, App Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
US-09-107-433-4519 US-09-710-279-1888 US-09-107-5514-519 US-09-107-5514-5119 US-09-102-540-9745 US-09-302-548-159 US-09-302-628-159 US-09-489-038,-1305 US-09-489-038,-1319 US-09-489-038,-13270 US-09-489-039,-13270 US-09-489-039,-13270 US-09-218-35-7262 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1 US-09-150-867-1
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ALIGNMENTS

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SULT 1 -09-830-217-16 Sequence 16, Application US/09830217 Patent No. 6521441 GENERAL INFORMATION: APPLICANT: Human Genome Sciences, Inc. APPLICANT: Human Genome Sciences, Inc. TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides FILE TREFERENCE: B846.PCT CURRENT APPLICATION NUMBER: US/09/830,217 CURRENT APPLICATION NUMBER: PCT/US99/06199 PRIOR FILING DATE: 1999-03-18 PRIOR FILING DATE: 1998-04-01 PRIOR FILING SATE: 1998-04-01		8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVLEYS	FVI	128 NNRHKGIYKDLANKIAPTIELKSFDGDYNENIDAFKTISKALGKEBEGKRLEEHDKKIEE 187 ::: :	X :: 5	8-8	293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
SULT 1 -09-830-217-1, Sequence 16, Sequence 16, Sequence 16, Series Information of the sequence 1711LE REPERENT FILLING PRIOR FILLING PRIOR PELING PRIOR PELING PRIOR FILLING NUMBER OF SEG 1D NO 16 LENGTH; 330 CREANISM; SOFTWARE: PART ORGANISM; SORGANISM; SOR	tch al Sim 113;	8 5	63	128	188	241	293
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RESULT 1 US-09-830-217-16 Squence 16, Application US/09830; Patent No. 6221441 GENERAL INFORMATION: APPLICANT: Human Genome Sciences TITLE OF INVENTION: Staphylococci; FILE REFERENCE: PB461PCT CURRENT APPLICATION NUMBER: US/0; CURRENT RILING DATE: 2001-04-24 PRIOR PILING DATE: 1999-03-18 PRIOR FILING DATE: 1999-03-18 PRIOR FILING DATE: 1999-03-04-01 PRIOR FILING DATE: 1998-04-01 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 SCPTWARE: Patentin Ver. 2.0 SCPTWARE: Patentin Ver. 2.0 LENGTH: 330 TYPE: PRT CRENTER: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: Patentin Ver. 2.0 LENGTH: 330 TYPE: PRT CRENTER: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 22 SCPTWARE: PATENTING DATE: 1998-05-07	A B B	& 원	상 임	<u>ک</u> ۾	දු පු	상 음 당	à
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                                                                                                                                    Indels
                                                                                                             293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sciences, Inc.
                                                                                                                                                                                                                                                               Sequence 5193, Application US/08781986A
Fatent No. 6737248
GENERAL INFORMATION:
TITLE OF INVENTION: Staphylococcus aur
TUMBER OF SEQUENCES: 5.255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MENJUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TOTAL STATEMENT (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Scies
STREET: 9410 Key West Avenue
CITY: Rockville
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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113; Conserv
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                                                                                                                                                                                                                   Patrick S. Dillon
Craig A. Rosen
Staven C. Barash
Michael R. Fannon
TILE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION TO DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. HYMEN
REGISTRATION NUMBER: 46,789
REPERRENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5193:
                                                                                                        Sequence 5193, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
G11 H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                        US-08-956-171E-5193
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ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

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Sequence 4516, Application US/09107532A
Patent No. 6581275
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 NNRHKGIYKDINKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL-----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                              APPLICANT: Simpson et al.
APPLICANT: Simpson et al.
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: Babaluson
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 69/830,217
PRIOR PILING DATE: 1999-06199
PRIOR PLING DATE: 1999-03-18
PRIOR PLING DATE: 1998-03-03
PRIOR PLING DATE: 1998-03-04
PRIOR PLING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: US 60/080,296
PRIOR PLING DATE: 1998-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.0%; Score 405; DB 4; Length 330; 32.8%; Pred. No. 1.9e-25;
                                                                          293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                 289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL-
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                                                                                                                                                                                          US-10-278-946-16
; Sequence 16, Application US/10278946
; Patent No. 6821754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
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LENGTH: 330
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SKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDG-----DYNENIDAFKTISKALGKE 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 --DDQ1EASTHGQS------VSYEYVLEKNPD1LFVVDRTKAIGGDDSKDDISANEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VRGLKILSVIGLLFVLIATAACG--NNSSSNSSKESS---KDGVEIKHEEG-TTKVPKHP
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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Best Local Similarity 31.3%; Pred. No. 2.2e-17
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...352
; SEQUENCE DESCRIPTION: SEQ ID NO: 4516:
US-09-107-532A-4516
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                       COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4516:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-8277
                                                                                      CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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17
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                                                                                                                                                                                                                                                                                                                                               179 EEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                       263 GSHGNI-----VNSELLLKINPDWMFVIDRDAAIGREDSQPA-KQVLDNALVRKVNAWN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 GLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVWKKLNAVK 294
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Fatent No. 6703492
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 1090-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 462
LENGTH: 347
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                                                                                                                                                          ----EGTTKVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                        34;
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                                      Score 296; DB 4; Length 351;
Pred. No. 2e-16;
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28.5%; Pred. No. 4.1e-16;
tive 68; Mismatches 121; Indels
                                                                                     66; Mismatches 118; Indels
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                                          17.5%;
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                                 Query Match
Best Local Similarity 29.24
Matches 90; Conservative
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US-09-543-681A-6862
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Best Local
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Patent No. 6605709

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 00/109/543, 681A
CURRENT PILING DATE: 2000-04-05
CURRENT PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6862
                                                                                                      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT FILING DATE: 1998-08-13 CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR PILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 5492 LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KIGKYTSVGTRKOPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 BFKDDKYINTGNLKEVNFDKVASAKPDVIFISGRTANQKNLDEFKKAAPKAKV-VYVGTS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 NENI--DAFK---TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVAHMKKTVLFLLSLVLVLTACSNSSNNNSTSKKKNSDSKETVTIKNSFEASGKENNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DONLIKDMKKNTENLGKIYDKEDKAKKINKDLDRKISDMKDK-TKDFNKKVMYLLVNEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKES-SKDGVEIKHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.5%; Score 296.5; DB 3; Length 3 Best Local Similarity 28.4%; Pred. No. 1.8e-16; Matches 104; Conservative 70; Mismatches 131; Indels
                                      ; Sequence 5492, Application US/09134001C; Patent No. 6380370; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Staphylococcus epidermidis US-09-134-001C-5492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 LVELSK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
U8-09-543-681A-6862
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Rockville
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                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 LVFDTLGFKPA------DKKVSKSPHGQNINNEYINKQNPDVILAMDRGSVVGGKATT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 RKQPNLEBISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENI--DAFK-- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 QFLSQLGFKEALSDDVTKGLSKYLKGPYLQ-MNTETLSQVNP-----ERMFIMTNKASS 273
                                      242 LVFDTLGFKPA------DKKVSKSPHGQNINNEYINKQNPDVILAMDRGSVVGGKATT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 KHPKRVVVLEYSFVDALVALDVKPVGIADDNK-----KORIIKPLRD--KIGKYTSVGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 -TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAH-PSNSYVG 220
                     --- ERMFIMTNKASS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LLFVLIATAACGNNSSSNSSKE----SSKDGVEIKHE-------EGTTKVP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                              Sequence 1268, Application US/09710279

Ratent No. 6703492

GRNERAL INFORMATION:
APPLICANT KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT APPLICATION NUMBER: 60164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2:1

SEQ ID NO 1268

LENGTH: 347
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                                                                                                         274 NEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Artificial Sequence: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.3%; Score 292; DB 4; Length 347; Best Local Similarity 28.5%; Pred. No. 4.1e-16; Matches 101; Conservative 68; Mismatches 121; Indels
                     221 QFLSQLGFKEALSDDVTKGLSKYLKGPYLQ-MNTETLSQVNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Arti: OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                         RESULT 9
US-09-710-279-1268
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Sequence 4342, Application US/09134000C

Batent No. 6617156
GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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122 I-SGRQQDYQEQLKAIAPTIYLAVDAKNPWASTKQNIETLGTI---FDKBEVAKEKITGL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGLSKYLKGPYLOMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LSVIGLLFVLJATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                          3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.7%; Score 283; DB 4; Lo
30.4%; Pred. No. 2e-15;
tive 59; Migmatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVIMLOPDVWYLSGGGLESMHL---MIEDVKK 314
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                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (301) 309-8504
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                  NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 101; Conservative
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                                                                    COMPUTER READABLE FORM
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Maryland
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US-09-071-035-40

Sequence 40, Application US/09071035

Sequence 40, Application US/09071035

Patent No. 64404040

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Bnterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                         288
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                                                 184 LATLNIVIEQAQKK-AAGSDKKVLVLLHNAGNLM--PNN-------QSVIYDVV 227
                                                                                                                                 81 GIADDNKKORLIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.9%; Score 268; DB 4; Length 296; Best Local Similarity 30.3%; Pred. No. 3.2e-14; Matches 96; Conservative 54; Mismatches 129; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                    287 TTSAYKNGGIVYLOSDLWYLSGGGLESLTQQIEAVQ 322
                                                                                                                                                                                           289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVE 324
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APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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APPLICANT: GARY BRETON
TITLE OF INVENTION: UDCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UDCASICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US /09/543,681A
CURRENT FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5565
LENGTH: 325
                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLII 125
                                                                                                                                                                                                                                                                                                                                                                                            : | : : | | | | | | | | :::
I-SGRQODYQEQLKAIAPTIYLAVDAKNPWASTKQNIETLGTI---FDKEEVAKEKITGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 ADNNRHKGIYKDLNKIAPTIEL ---- KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 HGQS-----VSYEYVLEKNPGILFVVDRTKAIGGDDSKDNVAANELIQKTDAGKND 291
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                                                                                                                                                                                                                                                                                                         17 VSMMGLLML----SACQTNKKTADSATTETTAKTEVTVKDTNGQLTVPKNPKKVVFDNG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
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                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        42;
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                                                                                                                                                                                         Query Match
16.7%; Score 283; DB 4; Length 327;
Best Local Similarity 30.4%; Pred. No. 2.1e-15;
Matches 101; Conservative 59; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5565, Application US/09543681A Patent No. 6605709
                                                                                                                             ORGANISM: Enterococcus faecalis
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4342
LENGTH: 327
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US-09-543-681A-5565
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Best Local Similarity 25.9%
Matches 82; Conservative
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ORGANISM:
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                                                      220 YEYVLEKNPGILFVVDRTKAIGGDDSKDNVAANELIQKTDAGKNDKVIMLQPDVWYLSGG 279
 NOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDD----VTKGLSKYLKGPYLOMN 252
                                          253 TETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRG 311
                     172 N-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEASTHGQS------VS
                                                                                                                                                                                                  APPLICANT: Kr"ger, Burkhard
APPLICANT: Sch"der, Hartwig
APPLICANT: Sch"der, Oskar
APPLICANT: Sch"der, Oskar
APPLICANT: Albertwer, Gregor
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REPERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT PILLING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-07-14
APPLICATION NUMBER: DE 19940764.9
FILING DATE: 1999-08-27
                                                                                                                                                            Sequence 572, Application US/09602787A Patent No. 6696561
                                                                                    312 LISSEEMAKELVELSKK 328
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280 GLESMHL---MIEDVKK 293
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APPLICANT: Pompejus, Mark
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US-09-602-787A-572
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Sequence 4860, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 TMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 TETLSQVNPERMFI-----MTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDL 305
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25.9%; Pred. No. 4.8e-14;
cive 60; Mismatches 135; Indels
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 1994036.5
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PLILNG DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR PLILNG DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR PRILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-31
PRIOR PRILING DATE: 1999-08-31
PRIOR PRILING DATE: 1999-08-31
PRIOR PRILING DATE: 1999-09-03
PRIOR PLILNG DATE: 1999-09-03
PRIOR PLILNG DATE: 1999-09-03
PRIOR PLILNG DATE: 1999-09-03
PRIOR PLILNG DATE: 1999-09-03
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PRIOR PRILING DATE: 1999-09-03
PRIOR PRILING DATE: 1999-09-03
PRIOR PLILNG DATE: 1999-09-03
PRIOR PRILING DATE: 1999-09-03
PRIOR PLILNG DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 678
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Sequence 2973, Application US/09583110

Sequence 2973, Application US/09583110

Sequence 2973, Application US/09583110

Sequence 2973, Application US/09583110

Sequence 2973, Application User all.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

FILE REFERENCE: DATE: US/09/583,110

CURRENT APPLICATION NUMBER: US/09/583,110

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 2973

SEQ ID NO 2973
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Patent No. 6800744;
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THAN TO THE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||:||:||:|||||||-----EKNIVGMPTKTVPTYLKDLVGTVKNVGFMKEPDLEAIAALEPDLIIASPRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 LIATAACGNNSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 LILLGACSTNSSTSQTETSSSAPTEVTIKSSLDEVKLSKVPEKIVTFDLGAADTIRALGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 321;
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AAKNGKIIQLTPDLWYLSGGGLESTKLMIEDIQKALK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 250; DB 4; 27.2%; Pred. No. 1.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae US-09-583-110-2973
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COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM
COMPUTER: <Unknown>
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Matches 92; Conservative
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US-09-107-433-4809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3723, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVALALGIVPVGFSKANYGVSADKGVLPWTEEKIKELNGKANLFDDLDGLNFEAISNSKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLIIADNNRHKGI----YKDLNKIAPTIELKSFDGDYNENI--DAFKTISKALGKEEEG- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLSQLG--FKEALSDDVTKGLSKYLKGPYLQMNTFTLSQVNPERMFIMTNKASSNEPSLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KKRLEEHDKKIEEYKKEITMDKNQKVLPAV---AAKSGLLAHPSNSYVGQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LIAILAMCIVFSACSSNSVKNEENTSKEHAPDKIVLDHAFGQTILDKKPERVATIAWGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 VIGLLFVLIATAACGNNS---SSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DALVALDVKPVGIADDN----KKNRIIKP-----LRDKIGKYTSVGTRKQPNLEEISKLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 ELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIRKRPVWKKLNAVKONORVDILDRDLAMARSRGLISSEEMAKELVELSKKDSKKDNK 60
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                                                                                                                                                                                                                                                                                                                                                                                  Length 60;
                                                                                                                                                                                                                                                                                                                                                                              th 15.7%; Score 265; DB 3; Similarity 92.9%; Pred. No. 6.3e-15; 52; Conservative 2; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 5322
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
LENGTH: 60
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                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
US-09-583-110-3723
                                                                                                                                                                                                                                                                                                           US-09-134-001C-4860
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Best Local
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Matches
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THILE REPERENCE: BG1-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/09/602,787A
PRIOR APPLICATION NUMBER: US 1991454.3
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-09
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R FILING DATE: 1999-07-09

R APPLICATION NUMBER: DE 1993229.5

R FILING DATE: 1999-07-09

R APPLICATION NUMBER: DE 19932230.9

R FILING DATE: 1999-07-09
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FILING DATE: 1999-08-27
PELLING DATE: 1999-08-27
FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940831.9
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PILING DATE: 1995-08-27
APPLICATION NUMBER: DE 19940765.7
FILING DATE: 1999-08-27
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APPLICATION NUMBER: DE 19940832.7
FILING DATE: 1999-08-27
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APPLICATION NUMBER: DE 19941378.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: DE 19941395.9
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FILING DATE: 1999-07-14
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FILING DATE: 1999-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE 1993227.9
FILING DATE: 1999-07-09
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FILING DATE: 1999-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 KPVGIADDNKKNRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LLLLGACSTNSSTSQTETSSSAPTEVTIKSSLDEVKLSKVPEKIVTFDLGAADTIRALGF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 LIATAACGNNSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV 77
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APPLICANT: Kr"ger, Burkhard
APPLICANT: Sch"der, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Jenderhauer, Gregor
TITLE OF INVENTION: CORYNEASCHERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapg
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14.8%; Score 250; DB 4; Length 325;
Best Local Similarity 27.2%; Pred. No. 1.1e-12;
Matches 92; Conservative 65; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 NAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: cUnknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...325
SEQUENCE DESCRIPTION: SEQ ID NO: 4809:
                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 598, Application US/09602787A Patent No. 6696561 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 325 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4809:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Sequence 70, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                       295
242
                                                                               291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 ----EBISKLKPDLIIADNNR--HKGIYKDLNKIAPTIELKSFDGDYNENI---DAFKTI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LKILSVIG--LLFVLIATAACGN-NSSSNSSKESSKDGVEIKHEEGTT-----KVPKHPK 59
                                                               243 -----QPISSEFIKKADPDILYIVDRTAVMEHRSNINAASV----ENPLLRQTKAMKO
186 QVKQV-QAVTANRPERALVVLHNNGAFSNFGIQSRYGFIFNAFGVKPASGVVDTSLHG--
                                       242 KYLKGPYLOMNTETLSQVNPERMFI-----MTNKASSNEPSLKELEKDPVWKKLNAVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LKKTVLIGTTLLLGSFLLAACGNTNKEANNADKT------HEVTDTLGNKVTVPAKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKALGKEBEGKKRLEEHD - - - KKIBEY - - KKEITMDKNOKVLPAVAAKSGLLAHPSNSYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486,33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                                                                                                 292 GRVIFVDADAWYTTAASPTSLKIVMEDVK 320
                                                                                                                           296 QRVDILDRDLWARSRGLISSEEMAKELVE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.3%;
Matches 98; Conservative 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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STATE: Maryland
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                                                                                                                                                                                                                                RESULT 21
US-09-071-035-70
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APPLICANT: Gary L. Brecon et al.

TITLE OF INVENTION: BACCON ET ALD AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4444
                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                          63 VLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKI--GK-YTSVGTRKQPNLEEISKL 119
                                                                                                                                                                                                                                                                                                                                                                       66 TLGVTDADIVLALGTVPVGNTGYKFFENGLGPWTDELVEGKELTLLDSDSTPDLEQVAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 LEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHP----SNSYV----GQFLSQLGF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 NEKTDALIQAAR-----DEN----PSFDGKTGTVILPYQGKYGAYLPGDARGQFLDSLGI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 LVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 KGIYKDLNKIAPTIELKSFDGDYNEN-----IDAFKTISKALGKEEEGKKRLEEHDK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|:|||||| :|:||||||| 139 UNQYQELSKIAPTIH---YDINFNNSESNHIGLVKDHMMTLGKIFNKEDLARQKVSELDE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIEBYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEA--LSDDVTKGLS 241
                                                                                                                                                                                                                                                                                                                                                                                                                            120 KPDLIIADNNRHKG-IYKDLNKIAPTIELKSFDGDYN-ENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 IGLLFVLIATAACGNNSSKSSKESSK--DGVEIKHEEGTTKVPKHPKRVVVLEYSFVDA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 SLPEAVLSRDTGDSF-----FVDVPAESVKDVDGDVLLVL----SNDENLDITAENP
                                                                                                                                                                                                                                                                                 7 KILRSSVVGVA-VLALLAGCSNNADDIDADSTSTGNSAFPVSIEHEFGTTTIDDVPERVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KIL--SVIGLLFVLIATAACGNNS----SSNSSKESSKDGVEIKHEEGTTKVPKHPKRVV
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.3%; Score 241; DB 4; Length 324;
Best Local Similarity 24.0%; Pred. No. 6e-12;
Matches 79; Conservative 77; Mismatches 135; Indels 38;
                                                                                                                                                                       Length 332;
                                                                                                                                                                 ch 14.6%; Score 246.5; DB 4; Length 3 il Similarity 26.7%; Pred. No. 2.2e-12; 94; Conservative 70; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4444, Application US/09328352
Patent No. 6562958
                                                                                   TYPE: PRT
ORGANISM: Acinetobacter baumannii
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 678
SEQ ID NO 598
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-328-352-4444
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                                                                                                                                                                       Query Match
Best Local
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87 KKNRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLN 139
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                                                                --- AAKNGK 267
246 GPYLOMNTETLSOVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWKKLAAVKNOR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 NSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NSSTSQTETSSSAPTEVTIKSSLDEVKLSKVPEKIVTFDLGAADTIRALGF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
14.0%; Score 236; DB 4; Length 298;
Best Local Similarity 26.6%; Pred. No. 1.4e-11;
Matches 88; Conservative 65; Mismatches 112; Indels
                                     ::: |::::||::::|
217 ---QEVSFESVKEINPDILFVINRTLAIGGDNSSNDGVLENALIAETP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                 298 VDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                          268 IIQLTPDLWYLSGGGLESTKCMIEDIQKALK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marke.
REGISTRATION NUMBER: 41,971
REPERENCE/DOCKET NUMBER: PB340P3
TELECOWUNINCATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 24, Application US/09536784; Patent No. 6573082; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 298 amino acids
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                     RESULT 23
US-09-536-784-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQ-LGFK--EALSDDVTKGLSKYLK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
                                                                              203 FMVSDNRSSGTVLYQDLGLQ---VPKLVEEISKNATADWNQVSLEKLAELDADHIFLVNS 259
                                            ------GOFLSQ-LGFKEALSDDVTKGLSKYLKGPYLOMNTETLSQVNPERMFIMTN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                          270 KASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                   KKONRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: B8340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 24:
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NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 amino acids
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CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-961-083-24
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Best Local Similarity
Matches 88; Conserva
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                                                                                                                                                                                                                                                                                                                                             RESULT 22
US-08-961-083-24
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                                                                                                                                                                                                                                                                             Sequence 6014, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICATIVE LYIND DOUGETEE-Stamm et al
TITLE OF INVENTION: UNCLETC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812

SOFTHARE PATENTING DATE: 1997-08-15
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Squence 72, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCES: 496
CORRESPONDENCES: 910
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 LQ---VPKLVEEISKOATADWNQVSLEKLAELDADHIFLVNSDESA-----PLFQEAIW 260
                               77 VKPVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKQPNL-----EEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 NNR--HKGIYKDLNKIAPTIELKSFDGDYNENI---DAFKTISKALGKEEEGKKRLEEHD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 ---KKIEEY--KKEITMDKNQKVLPAVAAKSGLLAHPSNSYV------GQFLSQ-LG 227
246 GPYLQMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWKKLNAVKNQR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AACGNINKEANNADKI------HEVTDILGNKVIVPAKPKRIIA---SYLEDYLVALG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 FKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AACGN-NSSSNSSKESSKDGVEIKHEEGTT-----KVPKHPKRVVVLEYSFV-DALVALD
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                                                                                                                                        268 IIQLTPDLWYLSGGGLESTKLMIEDIQKALK 298
                                                                                                           298 VDILDRDLWARSRGLISSEEMAKELVELSKK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; Conservative
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Matches 92; Conserv
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US-09-071-035-72
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79 PVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKOPNL-----EEISKLKPDLIIADNN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 ALVEGGKYKEYSKIAPTYVVKN----GENVTWRDQLEDIATVLDKKEQAKKVLEDYDTL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 BALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELBKDPVWKK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 CGN-NSSSNSSKESSKDGVEIKHEEGTT----KVPKHPKRVVVLEYSFV-DALVALDVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 -KKIEEY--KKEITMDKNOKVLPAVAAKSGLLAHPSNSYV----
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectre 486/33
COMPUTER: HP Vectre 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPAVKNNOVHTYDK----KSSWLYNGPIANTQIVEDVKK 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%; Score 228; DB 4; 26.5%; Pred. No. 6.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09302626B
Patent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Rasignani, Vega
APPLICANT: Rasignani, Vega
APPLICANT: Rapuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TILE OF INVENTION: Meningococcal Antigens
FILE REPERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCS/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 289 amino acids
amino acid
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Best Local Similarity 26.5%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-071-035-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-302-626B-12
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246

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184 A-AKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGV-PAVDESIKEGSHCQ--- 238
                                                                                                                                                                                                                                                                                                                                                                                                                           247 PYLOMNTETLSQVNPERMFIMTNKASSNE--PSLKELEKDPVWKKLNAVKNQRVDILDRD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                       -IDAFKTISKALGKEEEGKKRLEEHDKKIE
                                                                                                                                                                                                               187 EYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 295;
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28.0%; Pred. No. 2.3e-09;
ive 53; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMB/KEY: misc_feature; LOCATION: (B) LOCATION 1...295; SEQUENCE DESCRIPTION: SEQ ID NO: 4519: US-09-107-433-4519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 TYLAAGG-----AQELLNASKQ 312
                                                HKGI YKDLNKI APTIELKSFDGDYNEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 LWARSRGLISSEEMAKELVELSKK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4519, Application US/09107433; Patent No. 6800744
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 295 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 4519:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM
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Best Local Similarity 28.00
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 HKGIYKDLNKIAPTIELKSFDGDYNEN----IDAPKTISKALGKEEEGKKRLEEHDKKIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 EYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 A-AKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGVPAV--DEAIK-----EG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 PYLQ-MNTETLSQVNPERMFIMTNKASSNE--PSLKELEKDPVWKKLNAVKNQRVDILDR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 SHGQPISFEYLKEKAYPDWLFYLDRSAAIGEEGQAAKDVLNNPLVAETTAWKKGQVVYLVP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | : | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 IATAACG--NNSSSNSSKE----SSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDA
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                                                                                                                                                                                                                                                                                                                                                                                                Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.9%; Score 218; DB 4; Best Local Similarity 27.1%; Pred. No. 4.7e-10; Matches 88; Conservative 63; Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09302626B
Patent No. 670966
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REPRENCE: CHROLIS9
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                    Neisseria meningitidis
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 321
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Best Local Similarity 26.2*
Matches 85; Conservative
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US-09-302-626B-10
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LENGTH: 321
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COMPUTER READABLE FORM:
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US-09-134-001C-5667
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                                                                                                                                                                                                                                                                                          69 VDALVAL----DVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQ-----PNLEEISKL 119
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                                                                                                                                   DLIIADNNRHKGI----YKDLNKIAPTIELKSFDGDYNENI--DAFKTISKALGKEEEG- 174
                                                                                                                                                                                                                                                                     FLSOLG--FKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLK 279
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                     10 LIAILAMCIVFSACSSNSVKNBENTSKEHAPDKIVLDHAFGQTILDKKPERVATIAMGNH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PARCEIL VOIT: 2.1
SEQ ID NO 1888
LENGTH: 299
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                                                                DALVALDVKPVGIADDN---KKNRIIKP-
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Patent No. 6703492
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US-09-710-279-1888
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Best Local S:
Matches 79
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Sequence 5667, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: BEIDERMIDS FOR DIAGNOSTICS AND THERABEUTICS
TITLE OF INVENTION: BOOSTICS AND THERABEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14

NUMBER: OF SEQ ID NOS: 5674

LENGTH: 309
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Sequence 583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 VDALVAL----DVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQ-----PNLEEISKL 119
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.2%; Score 205.5; DB 3; Best Local Similarity 25.2%; Pred. No. 4.8e-09; Matches 79; Conservative 62; Mismatches 111;
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ORGANISM: Staphylococcus epidermidis
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CITY: Waltham
STATE: Massachusetts
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264 AVKNTRIETVDGD 276
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292 AVKNORVDILDRD 304
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72 LVALDVKPVGIADDNKKARIIKPLRDKIGKYTS-VGTRKQPNLEEISKLKPDLIIADNNR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 YVGOFLSQLGFKEAL--SDDVTKGLSKYLKGPYLQMNTETLSQV-----NPERMFIMT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| || |: |: || : :|| : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | : :|| | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 BLKHETGTLSVPATPSRLAVYDLGVLDTLNALGIRAVAVPK-----ATFPATLSAYN 76
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10.7%; Score 181.5; DB 4; Length 240;
Best Local Similarity 32.2%; Pred. No. 3.2e-07;
Matches 59; Conservative 34; Mismatches 67; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Description of Artificial Sequence: ORF38a
US-09-302-626B-159
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.9%; Score 185; DB 4; Length 316;
Best Local Similarity 22.8%; Pred. No. 2.4e-07;
Matches 64; Conservative 51; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 NKASS---NEPSLKELEKDPVWKKLNAVKNQRVDILDRDLW 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:: | | | :: | | | 323 RGAATGGGENKALETLAKHPELSQTRAFKQGRVIVVDAPSW 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Scalato, Enzo
APPLICANT: Scalato, Enzo
APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIROIS9
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT PILING DATE: 1999-04-30
PRIOR APPLICATION WUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9745
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Myxococcus xanthus US-09-902-540-9745
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LENGTH: 240
                                                                                                                                                                                                                                                                        LENGTH: 316
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
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Best Local Similarity 23.4%; Pred. No. 4.4e-08;
Matches 78; Conservative 69; Mismatches 107; Indels 79.
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                                      CUMPUTER: CUINCH ISCORD
COMPUTER: PC
COUNCH
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
RECISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...338

SEQUENCE DESCRIPTION: SEQ ID NO: 5819:
US-09-107-532A-5819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (701)893-5007
TELEPAX: (781)893-507
INFORMATION FOR SEQ ID NO: 5819:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acids
                   MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
US-09-902-540-9745
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

GATY Brecon et. al

APPLICANT:

GATY Brecon et. al

TITLE OF INVENTION:

PURCHINON: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

TOP-2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 RKQPNLEEISKLKPDL-------145
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                                                                                                                                                                                                                                                                                                                                                                          Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                     62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 HKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISK 166
                                                                                                                                                                                                                                                                                                                                                                       Query Match
9.1%; Score 153; DB 4;
Best Local Similarity 30.1%; Pred. No. 4.3e-05;
Matches 47; Conservative 31; Mismatches 62
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7331, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                     ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                          ; LOCATION: (142) .. (143)
; OTHER INFORMATION: unknown
US-09-302-626B-8
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Matches 69; Conserv
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US-09-489-039A-7331
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                                                                                                                                                     LENGTH: 164
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gary Breton et. al TILLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO YOURDENING TO BE PILLE REFERENCE: 2709-2004001 CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT APPLICATION NUMBER: US/09/489,039A PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PLING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 LVALDVKPVGIADDNKKNRIIKPLRDKIG---KYTSVG-TRK------QPNLEBISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDLILVSATGGDSALPLYDQLKTIAPTLVINYDDKSWQTLLTQLGQIT---GHEQQASAR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19. IADFNKQLVSLKEKMKLPPQ----PVTALVYTAAAHSANIWTPESAQGQMLEQLGFSLAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSDDVTKGLSKYLKGPYLQMNTETLSQ-VNPERMFIMTNKASSNEPSLKELEKDPVWKKL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 LPGGLPASHSQGKRHDIVQLGGENLAAGLNGQSLFLF----AGDQKDADAIYANPLLAHL 302
       73 LSKLGVK-TGLSVD--KNRL--PYLEBYFKTTKPAGTLFEPDYETLNAYKPQLIIIGSRA 127
                                                       HKGIYKDLNKIAPTIELKSFDGDYNEN----IDAFKTISKALGKEEEGKKRLEEHDKKIE 186
                                                                                                  128 AKAFDK-LNEIAPTIEMTADTANLKESAKERIDA---LAQIFGKKAEADKLKAEIDASFE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSN----SYVGQFLSQLGFKEA- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 SVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%; Score 157.5; DB 4; Length 22.1%; Pred. No. 4.9e-05; tive 61; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 8 | Application US/09302626B | Patent No. 6709660 | GENERAL INPORMATION: GENERAL INPORMATION: APPLICANT: Scalato, Enzo APPLICANT: Masignani, Vega APPLICANT: Pizza, Mariagrazia APPLICANT: Pizza, Mariagrazia APPLICANT: Grandi, Guido ITIRE REPRENCE: CHIROLS9 | TITLE REPRENCE: CHIROLS9 | CURRENT APPLICATION NUMBER: US/09/302,626B
                                                                                                                                                                                                                                                                                                Patent No. 6610836
GENERAL INFORMATION:
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13095
LENGTH: 337
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Matches 68; Conserv
                                                                                                                                                                                                     184 AAK 186
                                                                                                                                                        187 EYK 189
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US-09-489-039A-13095
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US-09-302-626B-8
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Sequence 7262, Application US/09328352
Sequence 7262, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 LLKPDLVIVGSGQ-----TQTIELLRQFGIAVYVMESGTYKQVKEELSEIAILS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 QLGFKEALSDDVTKGLSKYLKGPY-----LOMNTETLSQVNPERMFIMTNKASSNE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 TVTVPLHPORIVSMHDLDITIPLIELGAPPIASHGRTRPDGSHYLRSSAQLTGVDFDNSD 143
                                                                                                                                                                                                                                                   89 NRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELK 148
                                                                                                                                                                                                                                                                                                                                                                                                                       207 KSG-LLAHPSNSYVGQFLSQLGFK-----EALSDDVTKGLSKYLKGPYLQMNTETLSQVN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| : | | :| | :| | :| | 242 NNGKVIVHHSYHALGRVLRDAGFRFPPLIERIPD-------GQRIDVSAEQLPELD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 FVDALVALDV--KPVGIADD-----NKKNRIIKPLRDKIGKYTSVGTRKQPNLEEIS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYV----GQFLS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: :: | |: |
183 GAQKRAQEILNFSDEIVAE--------VAAKTARQPNKQSIYYAWSGGRIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 IMKLLASLLTLLLLCGCSSSEQNRKTQENSTSHSICVFDSTNTKVCVAKPAQRIVSLFES
                                                                                                                                                                                                                                                                           10 ILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTK--VPKHPKRVVVLEYS
                                                                                                                                                                   --- GIADDNKK
                                                                                                                                                                                                                                                                                                                                       149 SPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKN--QKVLPAVAA
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                                                                                                                         63;
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                                                                               Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 140.5; DB 4; Length 3.; Pred. No. 0.0013; 56; Mismatches 113; Indels
                                                                                                                         Indels
                                                                                                                         90;
                                                                               DB 4;
                                                                           ; Score 143.5; DB 4
; Pred. No. 0.00079;
47; Mismatches 90
                                                                                                                                                                 51 TTKVPKHPKRVVVL-EYSFVDALVALDVKPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 PSL----KELEKDPVWKKLNAVKNORV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii US-09-328-352-7262
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 ADFVFATWRSDTGGKP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 PERMFIMTNKASSNEP 276
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                                                                                    8.5%;
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Best Local Similarity 22...
Best Tocal Similarity 22...
Then 75; Conservative
                                                                               Query Match
Best Local Similarity 21.9*
Matches 56; Conservative
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US-09-328-352-7262
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                                                                                                                                                                                         Sequence 12270, Application US/09489039A
Sequence 12270, Application US/09489039A
Patent No. 6610836
Patent Sequences Relating to Klebsiella
Title OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLER: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 7324

LENGTH: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 NPQVIFVQDRYPQ----VVXQIENDPQWQAIDAVKHHVWLMPE--YAKAWGYPMPEALA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IDVGLRTEPNLELLTQMKPSFIVWSAGYGPSPEK-LARIAPGRGFTFSDGKRPLAMAQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 FKTISKA--LGKEEEGKKKLEEHDKKIEEYKKEITMDKNQKVLP-AVAAKSGLLAHPSNS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 YVGQFLSQLGPKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 IFQEVI.DRFGIKNAWHGEAAFWGS------VSVGIDRLAAFNEADVICFDH---GNERD 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CPGDAGGTDAQRHS--GTDLRHPDGDPATPGRCGAGKLCLLMMNPTLITRRRLLIAMALS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
8.5%; Score 144; DB 4; Length 353;
Best Local Similarity 20.9%; Pred. No. 0.00067;
Matches 67; Conservative 52; Mismatches 137; Indels
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357 LGELWMAKK 365
                                                                  320 KELVELSKK 328
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US-09-489-039A-12270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 353
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276 PKLIYERKELQ-----GLSAVQNRKV 296

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US-UB-951-083-194

| Sequence 194, Application US/08961083 |
| Sequence 194, Application US/08961083 |
| Patent No. 615946 |
| Patent No. 615946 |
| Patent No. 615946 |
| GARBERAL INCRAMITIC CHOIGE. |
| TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 |
| CORRESPONDENCE ADDRESS: 452 |
| CORRESPONDENCE ADDRESS: 452 |
| STREET: 9410 KW West Avenue |
| COMPUTER: MADYLE FORM: MADOS version 6.2 |
| COMPUTER: READABLE FORM: MSDOS version 6.2 |
| COMPUTER: BADIL TATE: MSDOS version 6.2 |
| COMPUTER: BADIL TATE: MSDOS version 6.2 |
| COMPUTER: MSDOS version 6.2 |
| SEPTING DATE: MSDOS version 6.2 |
| PILING DATE: MSDOS version 6.2 |
| FILING DATE: MSDOS version 6.3 |
| FILING DATE: MSDOS ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 IATAACGNNS---SSNSSKESSKDGVEIKHEEGTIKVPKHPKRVVVLEYSFVDALVALDV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IVFSACSSNSXKNEENTSKEHAPDKIVLDHAFGQTILDKKPERVATIAWGNHDVALALGI 61
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7.9%; Score 134; DB 3; Length 132;
Best Local Similarity 30.5%; Pred. No. 0.0012;
Matches 39; Conservative 23; Mismatches 52; Indels
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MOLECULE TYPE: protein
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OM protein - protein search, using sw model

August 25, 2005, 09:17:46; Search time 65 Seconds (without alignments) 2639:177 Million cell updates/sec Run on:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK 335 Title: Perfect score: Sequence:

Scoring table:

Searched:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 Total number of hits satisfying chosen parameters:

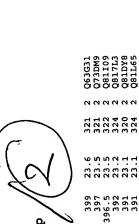
Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Q99889 staphylococ	Q7a499 staphylococ													-		photor				рвеифошоп				_	_	_			
SUMMAKIES			QBCNG3	688660	Q7A499	Q6GEQ2	QBNVD6	Q6G7D7	QBNXA6	Q6GAH5	Q99V55	Q7A6B6	Q6GI45	034348	919400	Q65LP5	Q9CPB7	Q8GRB3	Q87FM4	Q7M254	Q6D898	Q93F19	FECB ECOLI	Q889 <u>T</u> 6	Q65F62	087491	Q7A1Z7	Q7A2Y7	Q7A869	Q6GD10	Q6GKJ0	081785	
		DB	7	7	0	~	~	~	~	~	~	~	~	~	~	~	N	~	7	~	7	~	٦	~	~	~	~	N	~	~	7	7	
		Match Length	334	327	327	327	327	327	319	319	319	319	319	315	348	325	298	307	307	302	304	300	300	306	325	330	330	330	330	330	330	321	
•	* Query	Match	99.5	72.9	72.9	72.8	72.6	72.6	42.9	42.9	42.9	42.9	42.6	40.2	36.2	36.0	30.6	28.9	28.8	28.2	28.2	27.4	27.2	26.9		24.0		24.0	24.0	24.0		23.9	
		S	1681	1232	1232	1230	1227	1227	725.5		724.5			679.5	611	608.5	516.5	488.5	487.5	476	476	463	460	454.5	415.5	405	405	405	405	405	405	404.5	
	Result	No.	1	7	m	4	ß	ø	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	



Q63g31 bacillus ce	'3dm9 bacillus ce	li09 bacillus ce	1713 bacillus ce	11dy8 bacillus ce	1165 bacillus an	hcz7 bacillus th	Sne2 bacillus li	Sen6 bacillus li	738w0 bacillus ce	1xm98 clostridium	11r05 bacillus an	shja9 bacillue th	3bt9 bacillus ce	
59Ö	073	081	081	083	081	190	90	190 190	272	680	180	90	:90	
063G31	073DM9	081109	Q817L3	Q81DY8	Q81L65	O6HCZ7	Q65NE2	Q65EN6	Q738W0	08XM98	081R05	Q6HJA9	Q63BT9	
7	7	~	~	~	N	~	N	2	~	~	N	N	N	
321	321	322	324	320	324	324	315	315	321	316	320	320	320	
23.6	23.5	23.5	23.2	23.1	23.1	23.0	22.5	22.5	22.5	22.4	22.4	22.3	22.1	
399	397	396.5	392	391	391	389	380	379.5	379.5	378	378	377	373	
32	33	34	35	36	37	38	36	40	41	42	43	44	45	

ALIGNMENTS

																			ő	61	09	121	120	181	180	241	240	301	300
RESULT 1 QBCNG3 ID QBCNG3 PRELIMINARY; PRT; 334 AA. AC OBCNG3;	01-MAR-2003 (TrEMBLrel. 23, Created)	DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) DT 01-MAR-2004 (TrEMBLrel 26 Last annotation undate)	Ferrichrome ABC transporter.	_	Staphylococcus epidermidis.	OC Bacteria; Firmicutes; Bacillales; Scapnylococcus. Ox NCBI TaxID=1980.	Ξ	RP SEQUENCE FROM N.A.	KC 91KAIN-A1-C 12420; By Bykmad-13950922	Zhang YQ., Ren SX., Li HL., Wang YX., Fu G., Yang J.,	Qin ZQ., Miao YG., W	dF., od D., Danchin A., Ten	Staphylococcus epidermidis strain (A	Mol. Microbiol. 49:1577-1593	DR EMBL; AE016/50; AA005409.1; np go. go.oooggal. Briton ion transporter activity: IEA.	GO; GO: 0006827;	InterPro; IPR002491; Periple	KW COMDIECE Procedume. SQ SEQUENCE 334 AA; 37438 MW; 92C02D41A5ABAF33 CRC64;	Ouery Match Best Local Similarity 99.7%; Score 1681; DB 2; Length 334; Best Local Similarity 99.7%; Pred. No. 5.2e-84; Matches 333; Conservative 1; Mismatches 0; Indels 0; Gaps	Qy 2 VESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRV	Db 1 MESVRGLXILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTIKVPKHPKRV	Qy 62 VVLEYSFVDALVALDVKPVGIADDNKKARIIKPLRDKIGKYTSVGTRKQPNLEBISKLKP	Db 61 VVLEYSFVDALVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKP	Oy 122 DLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEH	Db 121 DLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH	OY 182 DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDVTKGLS	Db 181 DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKRALSDDVTKGLS	Qy 242 KYLKGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVMKKLNAVKNQRVDIL	Db 241 KYLKGPYLQMYTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDIL

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SEQUENCE FROM N.A.
STRAINS-MUSO / ATCC 700639;
MEDILINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
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0
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                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).

EMBL, AP003364, BAB58339.1; -.

PIR, D90013; D90013.

GO, GO:0005381, F:iron ion transporter activity, IEA.

GO, GO:0006537; P:high affinity iron ion transport; IEA.

Interpro, IPR002491, Peripla BP.

Pfam; PF01497; Peripla BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AA; 36591 MW; 6AEEECBC4E17CDB7 CRC64;
                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                              Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
DRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
           DRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 334
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                                                                                                                                                     OrderedLocusNames=SAV2177;
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Matches 235, Conservative
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                                                                               PRELIMINARY;
                                                                                                                                                                                       NCBI_TaxID=158878;
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SEQUENCE 327 AA
                                                                                          099589;
01-JUN-2001
01-JUN-2001
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302
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ID Q7A499
AC Q7A499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                 MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cul L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanto C., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shiba T., "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 BYSFADALAALDVKPVGIADDGKKKRIIKPVREKIGDYTSVGTRKQPNLEBISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theres, ", aureus, ", aureus, ", aureus, ", aureus, ", aureus, ", f. Lancet 357:1225-1240(2001).

R EMBL; AP003136; BAB43269.1; -.

R GO, GO:00061381; F:ixon ion transporter activity; IEA.

DR InterPro; IPR002491; Peripla_BP.

DR Pfam; PF01497; Peripla_BP_2; 1.

KW Complete proteome.

SEQUENCE 327 AA; 36591 MW; 6AEEECBC4E17CDB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transport system binding lipoprotein.
OrderedLocusNames=SAR2268;
(TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain MRSA252).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match / 72.9%; Score 1232; DB 2; Best Local Similarity 71.9%; Pred. No. 1.5e-59; Matches 235; Conservative 42; Mismatches 50;
                                                                                                                           Staphylococcus aureus (strain N315).
Bacteria, Firmicutes; Bacillales; Staphylococcus
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SEQUENCE FROM N.A.
PubMed=15213324; DOI=10.1073/pnas.0402521101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AA
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                                                                                                     OrderedLocusNames=SA1979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                 NCBI_TaxID=158879;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                             SA1979 protein.
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64 9 184

244

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RA Holden M.T.G. Fell E.J. Lindaay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Fell E.J. Lindaay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Fester T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Enright M.C., Corton C., Crillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher T., Lennard N., Line B., Hauser H., Holroyd S., Jagels K.,
Annes K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quall M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Marrell B.G.,
RA Spratt B.G., Parkhill J.;
RY Complete genomes of two clinical Staphylococcus aureus strains:
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT "Complete pright affinity iron ion transport; IEA.
DR GO: GO:0006827; P:high affinity iron ion transport; IEA.
RW Complete protecome: Lipoprotein.
SEQUENCE 327 AA; 36577 MW; GABCDBC4EI69CB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                          KGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                  125 IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKK
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                                                                                                                                                                                          Gaps
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                                                                                                                                         72.6%; Score 1227; DB 2; Length 327; 71.6%; Pred. No. 2.8e-59; ive 42; Mismatches 51; Indels (
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GO; GO:0006827; P:high affinity iron ion transport; IEA.
InterPro; IPR002491; Peripla_BP.
                                                                                              327 AA; 36577 MW; 6AEDCDBC4E169CB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Putative transport system binding lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain MSSA476).
Bacteria, Firmicutes; Bacillales, Staphylococcus
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PubMed=15213324; DOI=10.1073/pnas.0402521101;
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                   InterPro; IPR002491; Peripla
Pfam; PF01497; Peripla_BP_2;
Complete proteome.
SEQUENCE 327 AA; 36577 MW;
                                                                                                                                                                    71.6%;
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Best Local Similarity 71.6
Matches 234; Conservative
                                                                                                                                                                                               Matches 234; Conservative
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                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004
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                                                                                                                                                Query Match
                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD 304
                      Enright M.C., Foster T.J., Minusoy U.S., Feature, J. Akkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Barron A., Bason N., Bentley S.D., Chillingworth C., Croin C., Cronin A., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch B., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.;

"Complete genomes of two clinical Staphylococcus aureus strains: Travidence for the rapid evolution of virulence and drug resistance.";

"Froc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

EMBL; BX571856; CAG41246.1; -. 101:9786-9791(2004).

ROJ, GO:0005381; P:ingh affinity iron ion transport; IEA.

InterPro; IPR002491; Peripla_BP.

PR Pem, PFCH197; Peripla_BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Takeuchi F., Kanoda M., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EYSFADALAALDVKPVGIADDGKKKRIIKPVREKIRDYTSVGTRKQPNLEEISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYS FVDALVALDVKPVGI ADDNKKNRI I KPLRDKI GKYTS VGTRKQPNLEEI SKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
         Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8%; Score 1230; DB 2; Length 327; Best Local Similarity 72.2%; Pred. No. 1.9e-59; Matches 236; Conservative 39; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         327 AA; 36687 MW; AC34D0F769D71265 CRC64;
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EMBL; AP004829; BAB95968.1; -.
GO; GO:0005381; F:iron ion transporter activity; IEA.
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW2103 protein.
OrderedLocusNames=MW2103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome SEQUENCE 327 AA
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Q8NVD6

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73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLIIADNNRHK 132
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EQSTLKSAFAFGISRAGMFINNEDTFWGQFLLKWGIQPEVTKDKTTHVGERKGGPYIYLN
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                                                                                              253 TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transport system extracellular binding lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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Pred. No. 5.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                      319 AA
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                                                                                                                                                                                                                         311 GLISSEEMAKELVELSKK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=SAS0973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                             61 EYSFADALAALDVNPVGIADDGKKKRIIKPVREKIGDYTSVGTRKQPNLEEISKLKPDLI 120
                                                                                                                                                                                                                                                                                     IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGPYLOMNTETLSQVNPERMPIMTNKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRD 304
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                                                                              VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                EYSPVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI
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MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
'Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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Lancet 359:1819-1827(2002).
Lancet 359:1819-1827(2002).
GO:0006819: Bab94786.1;
GO:0006827; P:high affinity iron ion transport; IEA.
GO:0006827; P:high affinity iron ion transport; IEA.
InterPro; IPR002491; Peripla_BP.
Pfam; PF01497; Peripla_BP_2; 1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
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SEQUENCE 319 AA
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                               MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani M.; Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Hukhle genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: :| :::| | || || : EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
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Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 319;
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            Last annotation update)
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
                                                                                                                        Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 724.5; DB 2
46.9%; Pred. No. 6.5e-32;
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GIIASESMAEDLEKIAEK 317
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05-JUL-2004 (TrEMBLrel. 27,
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Matches 149; Conservative
                                                          SA0891 protein.
OrderedLocusNames=SA0891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MNSO / ATCC 700699;
MEDLINE=2131952; Pubmed=11418146; DOI=10.1016/SO140-6736(00)04403-2;
MEDLINE=2131952; Pubmed=11418146; DOI=10.1016/SO140-6736(00)04403-2;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Matcori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 VVFMLILVVVAVAGGGGKDT-----EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
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EMBL, AP003361; BAB57200.1; -.

PIR; B89872; E89872.

GO, GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0006827; P:high affinity iron ion transport; IEA.

InterPro; IPR002491; Peripla BP.

Pfam; PF01497; Peripla BP.
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                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (etrain Mu50 / ATCC 700699).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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(TrEMBLrel. 27, Last sequence update)
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                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequenc)
01-WAR-2004 (TrEMBLrel. 26, Last annotation of the control of 
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GIIASESMAEDLEKIAEK 317
                             300 GIIASESMAEDLEKIAEK 317
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Best Local Similarity 46.9
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 KIKBELSKIAPTIMLVSGTGDYNANIEAPKTVAKAVGKEKEGEKRLEKHNKILAEIRKKI 183
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RA Beson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
A Ormond D., Quail M.A., Rabbinowitsch E., Ritherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
R. Complete ganomes of two clinical Staphylococcus aureus strains:
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T. "Complete Proteone":
T. "RENBL: Pariple Affailty iron ion transport; IEA.
T. "Therepro; IER002491; Periple BP."
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T. "Therefore Transporter activity; IEA.
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T. "Therefore Transporter activity is the Complete Transporter activity is the C
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MEDLINE=96944033; PubMed=9384377; DOI=10.1038/36786;
MEDLINE=96944033; PubMed=9384377; DOI=10.1038/36786;
Kunst F., Ogssawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessiers P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ertlich S.D., Emmerson P.T.,
Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujta M., Pujta Y., Funa S., Gallazi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                       42.6%; Score 719.5; DB 2; Length 319;
46.2%; Pred. No. 1.2e-31;
Live 65; Mismatches 95; Indels 11.
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Name=yfmC, OrderedLocusNames=BSU07520;
Bacillus subtilis.
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GIMASESMAEDLEKIAEK 317
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01-JAN-1998 (TEMBLrel. 05,
01-JAN-1998 (TEMBLrel. 05,
25-OCT-2004 (TEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.2
Matches 147, Conservative
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WEDLINE=9417488; PubMed=9272861; DOI=10.1016/S0378-1119(97)00130-3;
Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;

"Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component of the Bacillus subtilis genome reveal genes for a new two-component of the Bacillus subtilis genome reveal genes for a new two-component of the Bacillus subtilis genome reveal genes for a new two-component of the Bacillus subtilis genome reveal genes for a new two-component of the Bacillus subtilis genome reveal genes for a new two-component of Gallis 12-199(1997).

RemBi, 299108; CAB12661.1; -.

REMBI, D86417; BAA22317.1; -.

REMBI, D86417; BAA22317.1; -.

RO, GO:0005381; F:iron ion transporter activity; IEA.

GO, GO:0005381; F:iron ion transporter activity; IEA.

InterPro; IPR002491; Peripla BP.

Remi; PR01497; Peripla BP.

Remi; PR01497; Peripla BP.

REMI; Complete proteome.

REMI; CAB1 REMI; C
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Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Klein C., Kobayashi Y., Koetter P., Kohingstein G., Krogh S.,
Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
Medique C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
A Medique C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
A Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
A Presort A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,
Rose M., Sadaie Y., Sato T., Scanlan E., Schleich B., Schroeter R.,
Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
A Shin B.S., Soldo B., Sorokin A., Taroconi B., Tarahashi H.,
Takemaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P.,
Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Yasumoto K., Yata K., Yoshika K., Yoshikawa H.P., Zumstein E.,
M. Mellandin A., Mandellandin A., Manane K.,
M. Masarotti A., Yoshika K., Yoshikawa H.P., Zumstein E.,
M. Manandin A., Manandin A., Manandin M., Manan
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"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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RFRGIKSSETSAKDVLK 310
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128 NNRHKGIYKDINKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
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Best Local Similarity 40.54
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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STRAIN=ATCC 14580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=279010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSM 13
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                                                                                                                                                                                                                                                                                                                REDLINES-98044033; Fubmace=9384377; DOL=10.1034/36/86;

KINDEL F. Ogasawara N. Mosesieres P., Bolotin A., Borchert S.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Broin S.Y., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Radiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Rilseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Allseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Allsert H., Holsappel S., Hascono S., Hullo M.F., Itaya M.,

Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,

A Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,

RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,

RA Kuein C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,

RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,

RA Rose M., Sadaie Y., Sarot T., Scanlan E., Schleich S., Schroeter R.,

Scoffone F., Sakiguchi J., Sekowska A., Seror S.J., Serror P.,

RA Rose M., Sadaie Y., Sarot T., Scanlan E., Schleich S., Schroeter R.,

Scoffone F., Sekiguchi M., Tanankoahi A., Taramata T., Tarahashi H.,

RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,

RA Wasaractti A., Wiari A., Wambutt R., Wedler E.,

RA Wasaractti A., Wiari A., Wambutt R., Wedler E.,

RA Wasanctti A., Wiari A., Wambute R., Walmane K.,

Rabaumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,

RA Woshikawa H., Danchin A., Yoshikawa H.F., Zumstein E.,

RA Woshikawa H., Danchin A., Toshikawa H.F., Zumstein E.,

RA Woshikawa H., Banchin Banchina B., Rapanort H.,

Rabaumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,

RA Washang K., Wata K., Yoshikaw H.F., Zumstein E.,

RA Washang K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Mismatches 109; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 348;
                                                                                                                                                                                                                          S:
                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                        Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO: GO:0005381; F: iron ion transporter activity; IEA.
GO: GO:0006827; P: high affinity iron ion transport; IEA.
Interpret; IPR002491; Peripla BP.
Pfam; PF01497; Peripla BP.
Complete proteome; Hypothetical protein.
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                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.2%; Score 611; DB 2;
41.2%; Pred. No. 1.1e-25;
                                                                                 Hypothetical protein yhfo.
Name=yhfo, OrderedLocusNames=BSU10330;
                                      Created)
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y14084; CAA74540.1; -. EMBL; Z99109; CAB12873.1; -.
                                 01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 25-OCT-2004 (TrEMBLrel. 28,
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     PRELIMINARY;
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                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                    Bacilius subtilis
                                                                                                                                                   NCBI_TaxID=1423;
                     O07616; Q796T6;
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                                                                                                                      303
                                                                                                                                                                                                                                     261 DSVNMGWTLEQLLKTDPDVIILMTGKTDDLDADGKRPIEKNVLWKKLKAVKNGHVYHVDR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the industrial bacterium Bacillus
licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004)
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247 --PYLOMNTETLSQVNPERMFIMTNKASSNEPSLKE-LEKDPVWKKLNAVKNQRVDILDR
                                                                                      188 YKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gustl V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen V.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
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; Pred. No. 1.4e-25;
69; Mismatches 118; Indels 7
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Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
Ehrenreich A., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-0CT-2004 (TTEMBLEC1. 28, Last sequence update)
25-0CT-2004 (TTEMBLEC1. 28, Last annotation update)
YhfQ (Aminotransferase, class-II).
Name-yhfQ; ORFNames=BL01086, BLi01111;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillus.
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EMBL, CP000002; AAU2571.1; -.
Andinotransferaes; Transferaes
SEQUENCE 325 AA; 35892 MW; 031DD170751A0577 CRC64;
                                                                                                                                                                                                                                                                                                                                  DLWARSRGLISS----EEMAKELVELSK 327
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                                                                 239 IKWTLEQLLEKDPDVIVLMTGEKDKVDEDGKRPIEKDPLWKKLSAVKNGKVYEADRFAWS 298
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181 KQKFG-SRKQSILLLGGNTNEEITVRDENFFTSQLLTKIGYTYGVGDS-GKGDAENGESVN 238
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                                            LOMNTETLSQVNPERMFIMT-NKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWA
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MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;

MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

MCOMplete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL, AE0066047; ARX02215.1;

GO, GO:0005381; F:iron ion transporter activity; IEA.

GO, GO:0006827; Pihigh affinity iron ion transport; IEA.

InterPro. IPR002491; Peripla BP.

Pfam, PP01497; Peripla BP.2; 1.

SEQUENCE 298 AA; 32954 MW; 55C1CA6834F1C490 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=fecB; OrderedLocusNames=PM0131;
Pasteuralla multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurallaceae; Pasteurella.
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01-MAR-2003 (TrEMBLrel, 23, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
Ferric vibrioferrin-binding periplasmic protein PvuB.
Name=pvuB;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                               298 AA.
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                                                                                                                                   308 RSRGLISSEEMAKELVE-LSKKDSKK 332
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01-JUN-2001 (
01-JUN-2003 (
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Matches
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Q9CPB7
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225 QLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSL-KELEK 283
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STRAINERIMD 2210633 / Serotype O3:K6;
STRAINERIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736 (03)12659-1;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736 (03)12659-1;
MAKINO K., OBAİMA K., KUROKAWA K., Yokoyama K., Uda T., Tagomori K.,
Iljima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancer 361:74-749(1003).
EMBL; AP005089; BAC62998.1; -.
GO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 VGMRSQPSLEAIAVLKPDLIIADAERHRAIYQDLQRIAPTLLLKSRGETYQENLESAQKI
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                                                                                                                                                                                                                                                             DOI=10.1128/JB.185.23.6938-6949.2003;
Tanabe T., Funahashi T., Nakao H., Miyoshi S., Shinoda S.,
Yamamoto S.,
Identification and characterization of genes required for
blosynthesis and transport of the siderophore vibrioferrin in Vibrio
parahaemolyticus.";
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Vibrio parahaemolyticus.
Batceria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TaxID=670;
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
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EMBL, AB082122; BAC16540.1; -.

GO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0006827; P:high affinity iron ion transport; IEA.

InterPro; IPR0249:; Peripla BP.

Ffam; PF0149; Peripla BP. 2; 1.

SEQUENCE 307 AA; 34309 MW; F6D94659A46245A7 CRC64;
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Matches 106; Conservative
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FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 196 KNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTET 255
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                                                                                                                                                                                                                               16 LLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVAL
                                                                                                                                                                                                                                                                                               DVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIY
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Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
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luminescens.";

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                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photorhabus luminescens (subsp. laumondii).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                        23;
                                                                                                             DB 2; Length 307;
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                                                                  DDA125C81E0E1638 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
1ron(III) dicitrate-binding periplasmic protein FecB.
Name=fecB; OrderedLocusNames=plu4447;
                                                                                                             28.8%; Score 487.5; DB 2; 35.4%; Pred. No. 5.1e-19; iive 72; Mismatches 106;
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InterPro; IPR002491; Peripla_BP.
                   Pfam; PF01497; Peripla_BP_2; 1. Complete proteome.
                                                                  34185 MW;
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                                                                                                                                                            Matches 110; Conservative
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Best Local Similarity .
Marches 102; Conservat
                                                                    307 AA;
                                                                                                                                     Local Similarity
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43 VEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKY 102

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103 TSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFK 162
                                                                                                                                  163 TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOF 222
                                                                                                                                                                                                                                                                  223 ISQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELE 282
                                                                                                                                                                                                                                                                                                                                                                                                 24 VIVQDEQGSFILNTVPQRVVVLELSFADALAAINISPVGIADDNDPQRILITDVRQRIKPW
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PubMed=15263089; DOI=10.1073/pnas.0402424101;
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Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-007-2004 (TrEMBLrel. 28, Created)
25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last sequence update)
1ron(III) dicitrate-binding periplasmic protein.
Name=fecB; OrderedLocusNames=ECA1076;
Ewinia carotovora (subsp. atroseptica) (Pectobacterium atroseptic Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriales;
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EMBL, BX950B51; CAG739B7.1; -
GO, GO:0005381; Firon ion transporter activity; IEA.
GO; GO:0006537; P:high affinity iron ion transport; IEA.
InterPro; IPR002491; Peripla_BP.
Dfam; PP01497; Peripla_BP_2; 1.
Complete proteome.
SEQUENCE 304 AA; 33394 MW; A280B695134CCBA5 CRC64;
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36.2%;
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Best Local Similarity 36.2#
Matches 104; Conservative
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SVLAALGL-----SVPKPIN---NAPMASINLEQLLAINPOWLIVTHYR---EESIVKR 247
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21437601; PubMed=11553538;

DOI=10.1128/IAI.69.10.6012-6021.2001;
Luck S.N., Turner S.A., Rajakumar K., Sakellaris H., Adler B.;
"Ferric dictrate transport system (Fec) of Shigella flexneri 2a
"Ferric dictrate transport pathogenicity island carrying multiple
antiblotic resistance genes.";
Infect. Immun. 69:6012-6021(2001).
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                                                                                                                                                                                                                                                                                                  Gammaproteobacteria, Enterobacteriales;
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                                 LEKDPVWKKINAVKNORVDILDRDLWARSRGLISSEEMAKELVELSK 327
                                                   248 WQQDTLWNWLEAQQKQQIAAVDSNAWARMRGIFAAERVGSDTVKIFK 294
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PECB ECOLI STANDARD; PRT; 300 AA.

PECB ECOLI STANDARD; CAST, 300 AA.

01-APP 990 (Rel. 14, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

25-JAN-2005 (Rel. 46, Last annotation update)

Iron(III) dicitrate-binding periplasmic protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Mismatches 104; Indels
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF326777; AAL08454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
InterPort, IPROGE1; Peripla BP.
Pfan; PPO1497; Peripla BP. 2; 1.
SEQUENCE 300 AA; 33166 WW; 6E0B0CF5B99AAAD CRC64;
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Last annotation update)
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                                                                                                                                                                                             Created)
                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae, Shigella
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Bacteria, Proteobacteria,
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01-DEC-2001
01-JUN-2003
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Nucleic Acids Res. 23:2105-2119(1995).
-!-FUNCTION: Binds citrate-dependent iron(III); part of the binding-protein-dependent transport system for uptake of citrate-dependent 24 VQDEHGTFTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS 84 VGTRAQPSLEAIAALKPDLIIADSSRHAGVYIALQQIAPVLLKSRNRTYAENLQSAAII SA SA LOCATION: Periplasmic. Belongs to the bacterial extracellular solute-binding 45 IKHERGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS 160 Potential. Iron(III) dicitrate-binding periplasmic protein family 8.
SIMILARITY: Contains 1 iron siderophore/cobalamin periplasmic-binding domain. Nervo 197 SSEAVIG proteome; Iron transport; Periplasmic; Signal; Transport 16; Sevensive 580 220 ووډ Length 300; STRAIN=K12 / MG1655; MEDLINE=95334362; PubMed=7610040; Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L., Indels Standenmaier H., van Hove B., Yaraghi Z., Braun V.
"Nucleotide sequences of the feeBCDE genes and locat.
proteins suggest a periplasmic-binding-protein-dependen.
mechanism for iron(III) dicitrate in Escherichia coli.";
J. Bacteriol. 171:2626-2633(1989). Fe/B12 periplasmic-binding 8 L -> V (in strain B).
23 T -> M (in Ref. 1).
1 -> S (in Ref. 1).
33146 MW, 6024ED0F9CR2D0EA CRC64; 62; Mismatches 104; 27.2%; Score 460; DB 1; 35.5%; Pred. No. 1.6e-17; Escherichia coli. Bacteria; Proteobacteria; Gammaproteobacte? Enterobacteriaceae; Escherichia. protein. EMBL; U14003; AAA97186.1; ALT_INIT. EMBL; U00096; AAC77246.1; ALT_INIT. PIR; S56515; QRECD3. ECOGRASE; EB0283; --ECOGRAP; EQ10287; fecB. Name=fecB; OrderedLocusNames=b4290; STRAIN=K12; MEDLINE=89213950; PubMed=2651410; InterPro; IPR002491; Peripla BP. Pfam; PF01497; Peripla BP 2; 1. PROSITE; PS50983; FE BI2 PBP; 1. EMBL; M26397; AAA23762.1; -SUBCELLULAR LOCATION: SIMILARITY: Belongs to dest Local Similarity 35.5 Matches 100; Conservative 295 300 AA; Similarity SEQUENCE FROM N.A. SEQUENCE FROM N.A. 39 22 7 NCBI_TaxID=562; Blattner F.R.; VARIANT CONFLICT CONFLICT Complete SEQUENCE Query Match DOMAIN CHAIN + δ 셤 ઠે a ò

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Q65F62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADN 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 LOMNTETLSQVNPERMFIMTNK----ASSNEPSLKEL-EKDPVWKKLNAVKNQRVDILDR 303
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GEMVGKKREMQARLEQHKERMAQWASO--LPKGTRVAFGTSREQOFNLHTQETWTGSVLA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Iron(III) dicitrate transport system, periplasmic iron-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKV--PKHPKRVVVLEYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLACGLL-TLLASAA------OAAPIDIDDGOHKVHLPDTPKRVVVLEFSF
                                                                                 202 SLGL------NVPAAMAGASMPSIGLEQLLAVNPAWLLVAHYR---EESIVKRWOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muchall C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.W., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Bender C.L., White O., Fraser C.M., Collmer A.;

The complete genome sequence of the Arabidopsis and tomato pathogen Proc. Natl. Acad. Sci. US.A. 100:10181-10186 (2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Рвеидотопав вугіпдае (рv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005381; F:iron ion transporter activity; IEA. GO; GO:0006827; P:high affinity iron ion transport; IEA. InterPro; IPR002491; Peripla_BP. Pefam; PP01497; Peripla_BP_2; 1. Complete proteome. SEQUENCE 306 AA; 32872 MW; 371BA711BC7A6108 CRC64;
                                                                                                                                                                               249 DPLWQMLTAAQKQQVASVDSNTWARMRGIFAAERIAADTVKI 290
                                                                                                                                                       DPVWKKUNAVRNORVDI LDRDLWARSRGLI SSBEMAKELVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60; Mismatches 111;
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Best Local Similarity 34.6%; Pred. No. 3.2e-17;
Matches 112; Conservative 60; Mismatches 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=fecB; OrderedLocusNames=PSPTO0763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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DVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELE------KDPVW 287
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EMBL, AE017333; AAU42302.1; -.
EMBL, CP0000002; AAU24333.1; -.
EMBL, CP0000002; AAU24333.1; -.
SEQUENCE 325 AA; 36700 MW; 949283E3C6C24775 CRC64;
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В. В.
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Rey M.W., Ramalya P., Nelson B.A., Brody-Karpin S.D., Zaretsky J. Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen J. Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                 (TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Veith B., Herzberg C., Steckel S., Feesche J.,
Ehrenreich P., Baeumer S., Henne A., Liesegang
Ehrenreich A., Gottschalk G.;
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KKLNAVKTGNAHEVDDAIWTTAGGV 308
                                                                                                                                                                                                                                                                                                                YfiY (Periplasmic binding protein).
Name=yfiY; ORFNames=BL02129, BLi03475;
Bacillus licheniformis DSM 13.
                         275 DSWARNRGIMASEQIADDALAVLK 298
DLWARSRGLISSEEMAKELVELSK .327
                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

PubMed=14688077; DOI=10.1128/IAI.72.1.29-37.2004;

PubMed=14688077; DOI=10.1128/IAI.72.1.29-37.2004;

PubMed=14688077; DOI=10.1128/IAI.72.1.29-37.2004;

Rale S.E., Doherty-Kirby A., Lajole G., Heinrichs D.E.;

"Role of siderrophore blosynthesis in virulence of Staphylococcus "Role of siderrophore blosynthesis in virulence of Staphylococcus aureus: identification and characterization of genes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heinrichs J.H., Gatlin L.E., Kunsch C., Choi G.H., Hanson M.S., "Identification and characterization of SirA, an iron-regulated protein from Staphylococcus aureus."; J. Bacteriol. 181:1436-1443(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005381; F: iron ion transporter activity, IEA. GO; GO:0006827; P: high affinity iron ion transport; IEA. InterPro; IFR002491; Peripla BP. Promer PF01497; Peripla BP.
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Last annotation update)
                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                            Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of a siderophore.";
Infect. Immun. 72:29-37(2004).
EMBL; AF079518; AAC62496.1; --
EMBL; AY251022; AAP82062.1; --
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05-JUL-2004
05-JUL-2004
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SEQUENCE 3
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                                                                                                                                                                                                                                 Name=sirA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ATDVAVSLGVKPVGAVESWTQKPKPRYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
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                                                                                                                         MEDLINE=22040717; Pubmed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Naghai Y., Imama N., Asano K., Naimi T., Kuroda H., Cui L., Yamanoto K., Hiramatsu K., Haramatsu K., Hiramatsu K., Agenome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                            24.0%; Score 405; DB 2; Length 330; 32.8%; Pred. No. 1.7e-14;
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                                                                                                                                                                                                                                        Lancer 359:1819-1827(2002).
EMBL, AP004822; BAB93953.1; -.
GO, GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
                                                                                                                                                                                                                                                                                                                        Complete proteome; Lipoprotein.
SEQUENCE 330 AA; 36744 MW; 63710BA22B208F61 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                 Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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           Name=sirA; OrderedLocusNames=MW0088;
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                                                                       NCBI_TaxID=196620;
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                           acquired MRSA."
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Q7A2Y7
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5 IKML-VVTLAFLLV-LAGCSGNSNKQSSDNKDKETTSIKHAMGTTEIKGKPKRVVTLYQG
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Best Local Similarity 32.8°
Matches 113; Conservative
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                                                                                                                                                                                         8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHBEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Maramorzi M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanenisa M., Vamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Mhole genome sequencing of meticillin-resistant Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                           179 FQK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAGEILNDLGFKR-----NKDL
                                                                                                                                          Gaps
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                                                                                                                                          34;
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                                                                                                             Length 330;
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                                                                                                                                        65; Mismatches 132; Indels
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GO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
                    EMBL; AP003358; BAB56277.1; -. GO; GO:0005381; F:iron ion transporter activity; IEA. GO; GO:0006827; P:high affinity iron ion transport; IEA.
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                                                                 Complete proteome; Lipoprotein. SEQUENCE 330 AA; 36744 MW; 63710BA22B208F61 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
                                                                                                           Query Match
24.0%; Score 405; DB 2;
Best Local Similarity 32.8%; Pred. No. 1.7e-14;
Matches 113; Conservative 65; Mismatches 132,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 AA
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Name=sirA; OrderedLocusNames=SA0111;
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Matches 113; Conservative
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Best Local Similarity
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SEQUENCE 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293
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63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEBISKLKPDLIVAS 122
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                                           63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                      128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
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FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD 127
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PubMed=1521324; DOI=10.1073/pnas.0402521101;

An Baright M.C., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,

An Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

Bason N., Bentley S.D., Chillingworth T.,

Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

An Eltwell T., Hanne Z., Harris B., Moule S., Mungall K.,

James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

Andres K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

Andres K.D., Parkhill J.; Stevens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J.; Stevens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J.;

T. Complete genomes of two clinical Staphylococcus aureus strains:

T. Complete genomes of two clinical Staphylococcus aureus strains:

T. Proc. Natl Acad. Sci. U.S.A. 101:9786-9791(2004).

RMBL, BX571857; CAG41856.1;

RO; GO:0005381; Fiton ion transporter activity; IEA.

GO; GO:0005381; Fiton ion transporter activity; IEA.

RICHERO, Peripla Affinity iron ion transport; IEA.

Reference of the Propial B.P. 2: 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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STRAIN=Sterne;
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Q81V85; (
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                             119 FOX----DAKAKYKDAWPLKASVVNPRADHTRIYAGGYAGEILNDLGFKR-----NKDL 228
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PubMed=15213224; DOI=10.1073/pnas.0402521101;
PubMed=15213224; DOI=10.1073/pnas.0402521101;
Partial M.T.G., Fester T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth T., A. Chillingworth T., Pance C. Clark L., Corton C., Chillingworth T., Pance C., Tarris B., Hauser H., Hollroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Spratt B.G., Parkhill J.;
Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RMBL; BX571856; CAG39144:1;
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RMBL; Proc. Natl. Peripla affinity iron ion transport; IEA.
Proc. Proc. Pring affinity iron ion transport; IEA.
Proc. Proc. Pring affinity iron ion transport; IEA.
Proc. Proc. Proc. Pringla BP-2:1.
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32.8%; Pred. No. 1.7e-14;
live 65; Mismatches 132; Indels 34; Gaps
                                                                                                                                     289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                       293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
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                                                                                                                                                                                                                                           05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                             Names Bring, OrderedLocusNames=SAR0118;
Staphylococcus aureus (strain MRSA252).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
                                                                                                                                                                                                                   330 AA
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72 LVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRH 131
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SIGNIENCE FROM N.A.

STRAIN=Ames / isolate Porton;

X MEDLINE=22608444; PubMed=12721629; DOI=10.1038/nature01586;

A Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eieen J.A., Gill S.R.,

A Holtzapple E.K., Oketad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.T., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

A Benton J.L., Mahamoud Y., Jang L., Hance I.R., Radune D.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Berton M.C., Plaut R.D., Wolf A.M., Watkins K.L., Nietman W.C.,

A Bazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

A Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

T.The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Federova N.B.,
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                                                                                                                                                                                                                                                         081V85; Q613H2; Q6KX85; 01-UN-2003 (TrEMBLrel. 24, Created) 01-UN-2003 (TrEMBLrel. 24, Last sequence update) 01-CTT-2004 (TrEMBLrel. 28, Last annotation update) 15-OCT-2004 (TrEMBLrel. 28, Last annotation update) 15-OCT-2004 (TrEMBLrel. 28, Last in Compound Dinding protein. OrderedLocusNames=BA0615, BAS0581, GBAA0615;
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fedd Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.;
Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
   332
                                      289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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TIGR; BA0615; -.
TIGR; BA0615; -.
GO; GAA06181; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
COMPLETE: IPRO0491; Peripla BP.2; 1.
COMPLETE: TIGHT: PERIPLA BP.2; 1.
SEQUENCE 321 AA; 36302 MW; BB17CFF136D893CC CRC64;
293 VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKUNK
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                                                                                                                                                                                                                                                                                                                          296
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                                                                                                                                                                                                                                                         248 YLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEK----DPVWKKLNAVKNQRVDILDR 303
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kinaka R.,
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                                                                                                                                                                                                                                                                                           192 KVNOEISMVRFMPGDVRIYHGDTFSGVILKELGFKRPGDQNKDDFAERNVSK-----
KG1YKDLNK1APT1ELKSFDGDYNEN1DAFKT1SKALGKEEEGKKRLEEHDKK1EEYKKE
                                                                                                                          ITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKYLKGP
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K. Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K. Hitchrock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka F. Richardson P., Rubin B., Tice H., T. Tice H., T. Tice H., "Complete genome sequence of Bacillus thuringiensis 97-27.";
"Complete genome sequence of Bacillus thuringiensis 97-27.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017355; AAT62409:1;
GO; GO:0006827; P:iron ion transporter activity; IEA.
GO; GO:0006827; P:iron affinity iron ion transport; IEA.
InterPro; IPR002491; Peripla BP.
Pfam; PF01497; Peripla BP.2; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
1ron(III) dicitrate ABC transporter, periplasmic protein.
Name=fecB; OrderedLocusNames=BT9727_0525;
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larity 31.4%; Pred. No. 1.9e-14;
Conservative 73; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis (subsp. konkukkan),
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=180856;
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75 LGVKPVGAVKSWTGDPWYPHIKDKMKDVKVVGDEGQVNVETIASLKPDLIIGNKMRHEKV 134
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PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A.; Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Anginoli S.V., Kolonay J.F., Shores K.A., Edistoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
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                                                                                                                                                                                                                                                                                                                                                                                     C., Hill K
, Okinaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 321;
                                                                                                                                                                                                                                                                                                                   STRAIN=ZK;
Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S.,
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000001; AAU19116.1; -.
SEQUENCE 321 AA; 36315 MW; 0A1B4742B1AB7945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
23.6%; Score 399; DB 2; Length 32
Best Local Similarity 31.4%; Pred. No. 3.6e-14;
Matches 101; Conservative 71; Mismatches 122; Indels
                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Tron(III) dicitrate ABC transporter, periplasmic protein.
                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBI_TaxID=288681;
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Bacteria; Firmicutes; Bacillales; Bacillus
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                                                                                                                                                                           Name=fecB; ORFNames=BTZK0525;
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   PRELIMINARY;
                                                                                                                                                                                                             Bacillus cereus ZK.
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75 ELGVKPVGAVKSWTGDPWYPHIKDKMKDVKVVGDEGGVNVETIASLKPDLIIGNKWRHEK 134
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                                                                                                                                                                          74 ALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKG 133
                                                                                                                                                                                                                                                                                                                  192 DKVNQEISMVRFMPGDVRIYHGDTFSGVILKELGFKRPGDQNKDDFAERNVSK-----
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                                                                                               9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKD----GVEIKHREGTTKVPKHPKRVVVL
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorotha, Anderson I., Galleron N., Candelon B.,
Rapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Gecchkin Y., Pusch G., Haselkorn R., Fonstein M., Bhrlich S.D.,
Overbeek R., Kyrpides N.C.;
"Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthrais.";
           29;
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           73; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacilius aucustus.
Nature 423:87-91(2003).
EMBL; AB017012; AAP11437.1; ...
GO; GO:0005881; F:iron ion transporter activity; IEA.
GO; GO:0006821; F:high affinity iron ion transport; IEA.
InterPro; IRR008091; Ferrichrome_bind.
InterPro; IPR002491; Peripla_BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=BC4528;
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 WARSRGLISS ---- EEMAKELVE 324
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PRINTS; PR01715; FERRIBNDNGPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrichrome-binding protein.
           Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITM 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 DKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKYLKGPYLQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 MNTETLSQVNPERMFIMT-NKASSNEPSLKELEK----DPVWKKLNAVKNQRVDILDRDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ERISAMDGDVLFYFTFDKGNENKGS--ELEKEYINDPLFKNLNAVKNGKAYKVDDVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LLAFSLLLSACGKSNTKEDTKEDTKKEMITVEHAMGKTEVPANPKRVVILTNEGTEALLE 74
adaptations and a large plasmid related to Bacillus anthracis px01.";

Nucleic Acids Res. 32:977-988(2004).

EMBL, AE017266; AAS39516.1;

TIGR, BCE0683;

GO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0005381; F:iron ion transporter ion transport.

InterPro; IPR002491; Peripla_BP.

Pfam; PF01497; Peripla_BP_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                16 LLFVLIATAACGNNSSSNSSKE-SSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhatracharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
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Nature 423:87-91(2003).
                                                                                                                                                                                                                                                                                                                                                                         30;
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                                                                                                                                                                                                                                                                                                                     Length 321;
                                                                                                                                                                                                                                                                                                               23.5%; Score 397; DB 2; Length 32: 31.0%; Pred. No. 4.6e-14; ive 77; Mismatches 116; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mature AZESTON, AAP07634.1; -. BMB, AZESTON, AAP07634.1; -. GO: 00.05381; F: iron ion transporter activity; IEA. GO: 00.06827; P: high affinity iron ion transport; IEA. TOPATON: IPR02491; Peripla_BP.
                                                                                                                                                                                                                                                           321 AA; 36322 MW; ACDEA9056A566FA5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24, Last sequence update)
26, Last annotation update)
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Iron(III) dicitrate-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 100; Conserva
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Best Local Similarity
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SEQUENCE 321 AA
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081109
1081109
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SEQUENCE FROM N.A
                                                                                                                            NCBI_TaxID=1392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 KILSVIGLLFVLIATAACG-NNSSSNSSKESSKOGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKY
                                                EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MPIMTNKASSNEPSLKELEKDPVWK
                                 178 LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                         Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 320;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; Score 391; DB 2; Length 32 30.2%; Pred. No. 9.7e-14; Live 64; Mismatches 138; Indels
                                                                                                                                                                                                                                                                         Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005381; F:iron ion transporter activity; IEA. GO; GO:0006827; P:high affinity iron ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 AA; 36173 MW; 95ED63B62B07323F CRC64;
                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Iron(III) dicitrate-binding protein.
                                                                                                                      289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                 ELKPKKENKMYKLKGDTWIFG-GPESATSLATQVADV 319
                                                                                                                                                                                                 320 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AE017005; AAP09174.1; -.
                                                                                                                                                                                                                                                                 OrderedLocusNames=BC2208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 30.29
                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus anthracis.";
Nature 423:87-91(2003)
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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65 EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKOPNLEEISKLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Ames / isolate Porton;

X MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Tourasse N.J., Bisen J.A., Gill S.R.,

Nelson K.E., Tettelin H., Pouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

A Rolonay J.F., Beanan M.J., Dodson R.J., Brinkec L.M., Gwinn M.L.,

DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Mahamoud Y., Jiang L., Hakins K.L., Nierman W.C.,

A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

A slaberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

T. closely related bacteria.";
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin B., Tice H.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017038; AAP28458 1.; -.
EMBL; AE017334; AAT33889.1; -.
TIGR; BA4766; -.
TIGR; BA4766; -.
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                     081L65; Q6HSL7; O6KLM1;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Iron compound ABC transporter, iron compound-binding protein.
OrderedLocusNames=BA4766, BAS4424, GBAA4766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fed
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005381; F:iron ion transporter activity; IEA
GO; GO:0006827; F:high affinity iron ion transport;
InterPro; IPR008091; Ferrichrome_bind.
InterPro; IPR002491; Peripla_BP.
                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae;
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PRINTS; PR01715; FERRIBNDNGPP
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Matches 116; Conservative
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                                                                                                                                                                                                                                           Bacillus anthracis.
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PubMed=15383718;
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Q65EN6
                                                 RESULT 39
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                                                                                                LEEHDKKIEEYKKEI ----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                              230 EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDLIITASFRGKAIKNELEGIAPTVMFDPSTSNNDHFAEMTETFKQIAKAVGKEEEGKKV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LADMDKA PADAKAKI EKADLKDKNI AMAQA PTAKNV PTFRILT--DNSLALOVTKKLG-- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LINTERAGKSE---PDGFKQTTVESLQSVQDSNFIXIVADEDNIFDTQLK---GNPAWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richhardson P., Rubin E., Tice H.;

"Complete genome sequence (B Bacillus thuringiensis 97-27.";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, ABC11355, AAT60882.1;

GO, GO:0005381; F:iron ion transporter activity; IEA.

GO, GO:0005381; P:high affinity iron ion transport; IEA.

InterPro; IPR008091; Peritchrome_bind.

InterPro; IPR00491; Peripla BP.

Pfam; PF01497; Peripla BP. 2; 1.

PRINTS; PR01715; PERRIBNNGPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iron compound ABC transporter, iron compound-binding protein. Name=fhub; OrderedLocusName=Br9797, 4264; Bacillus thuringiensis (eubsp. konkukian). Bacteria, Firmicutes; Bacillas; Bacillus et Pirmicutes; Bacillas; Bacillas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.0%; Score 389; DB 2; Length 324; 34.1%; Pred. No. 1.3e-13; tive 60; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 AA; 36067 MW; 8B2335F21181CF5F CRC64;
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                                                                                                                                                                                                                                                                                    KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELKFKKENKMYKLKGDTWIFG-GPESATSLATQVADV 319
                                                                                                                                                                                                                                                        KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA
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Conservative 6
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Matches 115, Conserv
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QGHCZ7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:877-877(2004).

EMBL; AE017333; AEU34242.1; -.

EMBL; CP0000002; AAU22065.1; -.

SEQUENCE 315 AA; 34672 MW; E239649B55EB47DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 IE-GRQSEQYDEFKKIAPTIDIELDQKNYMNSFKENTE---NIGKIFGKEDAVKEALAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 DEKVEKANK-LAKEKGGKGLVVLTSDKQISAYGSGSRFGLIHDVLGV----EPVDKNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 KILSVIGLLFVLIATAACGNNSSSNSSKESS-KDGVEIKHEBGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 FVDAL -- VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zaretsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 14580,
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                   Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.
Ehrenreich A., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
YClQ (Periplasmic binding protein).
Name=yClQ; ORFNames=BL01760, BLi00466;
Bacillus licheniformis DSM 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.5%; Score 380; DB 2; I 32.8%; Pred. No. 3.8e-13; Live 64; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 AA.
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25-OCT-2004 (TrEMBLrel. 28, Created)
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                             NCBI_TaxID=279010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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ug-10-724-972a-6352.rup

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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 IIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 KIBEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGF---KEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SKYLKGPYLQMNTETLSQVNPERMFIMT-----NKASSNEPSLKELEKDPVWKKLNAVKN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VRGLKILSVIGLLFVLIATAACGNNSSSNSS-KESSKDGVEIKHEEGTTKVPKHPKRVVV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-R77(2004).

GENBL; AE017333; AAU42478.1; -.

EMBL; CP0000002; AMU25109.1; -.

Hypothetical protein.

SEQUENCE 315 AA; 34861 MW; F018C0B904038C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Gaps
                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenzeich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenzeich A., Gottschalk G.; The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Periplasmic binding protein).
ORFNames=BL03470, BL103657;
Bacillus licheniformis DSM 13.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.5%; Score 379.5; DB 2; Best Local Similarity 29.7%; Pred. No. 4e-13; Matches 97; Conservative 70; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 QRVDILDRDLWARSRGLISSEEMAKEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 GNVHKVSDAIWNTAGGVLAANLMLDDI 309
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                         PubMed=15383718;
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Search completed: August 25, 2005, 09:23:53 Job time : 71 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2005, 09:19:06; Search time 20 Seconds (without alignments) 1611.631 Million cell updates/sec Run on:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL......EEMAKELVELSKKDSKKDNK 335 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	hypothetical prote	ferrichrome ABC tr	iron(III) dicitrat	citrate-dependent	•		н	o.	a	î	iron(III) dicitrat	_	_		iron(III) dicitrat	periplasmic iron-c	hypothetical prote	iron(III) dicitrat	iron(III) dicitrat	Ē		iron(III) dicitrat	iron-uptake system	E	_			iron(III) dicitrat
ID	D90013	E89872	B69812	F69831	QRECD3	G89771 ·	C69805 ·	E83779	E69763	G84123	AH2128	AG2082	AG2129	S74458	AC2421:	AF2082	AC1855	A89846	AD2134	AD2082	AE2074	AD2085	AD2079	I39842	S32930	AG2075	T36412	AB2130	A11943
DB	2	7	-	-	-	N	Н	~	-	~	~	~	~	7	7	~	~	~	~	~	~	~	~	~	~	N	N	~	N
* Query Match Length DB	327	319	315	348	302	330	325	341	317	334	328	325	330	330	319	326	300	342	331	330	361			317	315	343	350	333	331
Query Match	72.9	42.9	40.2	36.2		24.0	22.1	20.7	19.7	19.7	19.3	18.3	17.5	17.3	17.1	17.0	16.9	16.9	16.8	16.5	16.4	16.4	16.4	16.4	16.3	16.2	16.2	16.2	15.8
Score	1232	724.5	679.5	611	460	405	373	350	332.5	332.5	327	310	295.5	292.5	288.5	288	285	285	284	279.5	278	277.5	277.5	276.5	275	274	274	273	267.5
Result No.	-	7	ო	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT

hypothetical prote	ferrichrome bindin	ABC transporter (b	enterochelin uptak	iron(III) dicitrat	hypothetical prote	hypothetical prote	iron(III) dicitrat	hypothetical prote	hypothetical prote	hypothetical prote	B. subtilis ferric	ABC transporter, s	conserved hypothet	iron(III) dicitrat	ferrichrome bindin	
B86666	AG1319	D70074	H81279	S74441	B95119	F97988	AF2130	G95218	E98082	D83778	AG1378	AG2880	939265	AB2078	AG1691	
~	~	~	~	Н	N	~	7	~	N	~	~	0	0	~	0	
313	313	319	330	315	341	341	349	321	321	329	323	341	341	322	313	
15.7	15.7	15.5	15.4	15.4	15.0	15.0	15.0	15.0	15.0	14.8	14.8	14.6	14.6	14.3	14.2	
265	264.5	261.5	261	260	254	254	254	253	253	250.5	249.5	246.5	246.5	242.5	240.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 D90013 D90013 D90013 C;Speciec C;Date: C C;Access R;Kuroda ma, A.; b C; Shi Lancet 3;A;Tete	n SA1979 [imported] - Staphylococcus a coccus aureus #sequence_revision 10-May-2001 #text_T; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, N.; Sawano, T.; Inoue tori, M.; Ogasawara, N.; Hayashi, H.; 40, 2001 me sequencing of meticillin-resistant A89758; MUID:21311952; PMID:11418146	ureus (strain N315) change 09-Jul-2004 1.; Kobayashi, I.; Cui, L.; Oguc 7, R.; Kaito, C.; Sekimizu, K.; Hiramatsu, K.
A;Accession A;Status: p A;Molecule A;Residues: A;Cross-ref A;Experimen C;Genetics: A;Genetics: A;Genetics:	A,Accession: DV013- A,Status: preliminary A,Molecule type: DNA A,Residues: 1-32-7 KUR- A,Experimental source: strain N315 A,Experimental source: strain N315 C,Genetics: A,Gene: SA1979 C,Superfamily: ferrichrome-iron transport protein fecB	177; PIDN:BAB43269.1; GSPDB:G
Query Best L	Query Match Pest Local Similarity 71.9%; Pred. No. 2.6e-62; Matches 235; Conservative 42; Mismatches 50; Indels	Length 327; Indels 0; Gaps 0;
& 8	5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEBGTTKVPKHPKRVVVL 	TTKVPKHPKRVVVL 64
ζ, d	65 EYSFVDALVALDVKPVGIADDNKKARIIKPLRDKIGKYTSVGTRKQPNLEBISKLKPDLI 	PNLEBISKLKPDL1 124 PNLEBISKLKPDL1 120
૪ ૦ .	125 IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKRLEEHDKK ::	KBEGKKRLEEHDKK 184 : : : KEKEGEKRLAEHDKL 180
& 5	185 IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGGFLSQLGFKEALSDDVTKGLSKYL :	SALSDDVTKGLSKYL 244 ALSDDVTKGLSKYL 240
ò 8	245 KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD :	.NAVKNQRVDI.LDRD 304
ò a	305 LWARSRGLISSEEWAKELVELSKKOSK 331 :	

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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local Similarity 41.2*
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 47.0%
Matches 149; Conservative
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                                             A; Molecule type: DNA
A; Residues: 1-315 < KUN>
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E89872
hypothetical protein SA0891 [imported] - Staphylococcus aureus (strain N315)
C, Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: E89872
C; Accession: E89872
R; Kurcda, M:; Othta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A: Milautani-Ui, Y:; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Accession: E89872
A; Status: preliminary
A; Molecule type: DNA
A; Readdues: 1-319 *KUR»
A; Readdues: 1-319 *KUR»
A; Cross-references: UNIPROT:Q99V55; GB:BA000018; PID:g13700840; PIDN:BAB42136.1; GSPDB:C
C; Genetics:
A; Gene: SA0891
C; Superfamily: ferrichrome-iron transport protein fecB
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C;Species: Bacillus subtilis
R;Kunst, F: Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Broni, S.; Brusillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
Nature 390, 249-256, 1997
Nature 300, 249-256, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::||:::||:::|| EQSTLK&AFAFGISRAGMFINNEDTFWGGFLIKMGIQPEVTKDKTTHVGERKGGPYIKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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42.9%; Score 724.5; DB 2; Length 319;
Best Local Similarity 46.9%; Pred. No. 8e-34;
Matches 149; Conservative 63; Mismatches 95; Indels 11;
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GIIASESMAEDLEKIAEK 317
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iron(III) dicitrate-binding protein homolog yhfg - Bacillus subtilis
CiSpecies: Bacillus subtilis
Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Cappano, V.; Carter, N.M.; ChO
A.; Erritch, S.D.; Emmerson, P.T.; Entini, M.D.; Errington, J.; Fabret, C.; Ferrari, E.
Naturhors: Foulgar, D.; Fritz, C.; Fulllar, M.; Fullta, N.; Masch, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Levine, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Levine, A.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, M.; Manuel,
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schlacto, S.; Schroeter, R.; Scoffone, R.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schlacto, S.; Schroeter, R.; Scoffone, F.; Sekfiguchi, J.; Sekowska, A.; Scanlon,
A; Minters, P.; Wipat, A.; Tanaka, T.; Tarpgerra, P.; Togano, A.; Tosato, V.; Uchiyama,
A; Hitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Attile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Attile: The complete genome sequence of the cram-positive bacterium Bacillus subtilis.
A; Attile: The complete genome sequence of the cram-positive bacterium Bacillus subtilis.
A; Attile: The complete genome contented to the cram-positive bacterium and the cram-positive bacterium preliminary.
A; Attile: The complete genome contented to the cram-positive bacterium and the cram-positive bacterium preliminary.
A; Attile: The complete genome contented to the characterium contented by the complete genome contented to the characterium and the complete genome contented to the 
A;Cross-references: UNIPROT:034348; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12581.
A;Experimental source: strain 168
A;Experimental source: strain 168
A;Genetics:
A;Genetics: Y#C
C;Superfamily: iron(III) dicitrate transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:007616; GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12873.
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEBISKLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NNRHKGIYKDINKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 YLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 YKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 611; DB 1; Length 348; ; Pred. No. 2.18-27; 68; Mismatches 109; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                     40.2%; Score 679.5; DB 1; Length 315; 47.0%; Pred. No. 2.6e-31; Live 50; Mismatches 103; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: yhfQ
C;Superfamily: iron(III) dicitrate transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSRGLISSEEMAKELVE 324
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Gaps

164

224 203

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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 1.0-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89771
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-330 «KUR»
A,Cross-references: UNIPROT:087491; GB.BA000018; PID:g13700031; PIDN:BAB41330.1; GSPDB:C
A,Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLGFKEALSDDVTKGLSKYLKGPYL-QMNTETLSQVNPERMFIMTNKASSNEPSLKELEK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Récresce number: A89758; MUID:21311952; PMID:11418146 A;Accession: G89771 A;Estatus: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKYLKG---PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL-----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                           SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS
                                                                                                                                                                                                                                                                                                                                                                                                 45 IKHEEGITKVPKHPKRVVVLEYSEVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                                        8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                         VGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
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                                                                 16;
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A;Gene: sirA
C;Superfamily; Bacillus subtilis ferrichrome ABC transporter fhuD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 330;
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      Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPVWKKINAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipoprotein [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.2%; Score 460; DB 1; L. L. L. S. S. S. S. Pred. No. 5.4e-19; Conservative 62; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 32.8%
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
Molecule type: DNA
Residues: 1-330 <KUR>
                                     Best Local Similarity
Matches 100; Conserv
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            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: JS0112
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 3-24, M'.26-58, S',60-302 <STA>
A,Exesidues: 3-24, M'.26-58, S',60-302 <STA>
A,Experimental source: strain K12
C,Comment: The sequence from strain B differs from that shown in having Val-10 and Thr-2
C,Comment: This protein is one of five, encoded by the fec operon, constituting a citrat G,Genetics:
A,Gene: fecb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-302 <BLAT>
A; Residues: 1-302 <BLAT>
A; Cross-references: GB:AE000499; GB:U00096; NID:g1790732; PIDN:AAC77246.1; PID:g1790742;
A; Experimental source: strain K-12, substrain MG1655
R; Staudenmaier, H.; Van Hove, B.; Yaraghi, Z.; Braun, V.
B. Barteriol. 171, 2626-2633, 1989
A; Title: Nucleotide sequences of the fecBCDE genes and locations of the proteins suggest
A; Reference number: PS0029; MUID:89213950; PMID:2651410
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-302/Product: iron(III) dicitrate transport protein fecB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVNNKATLEQLLKTDPDVIILATGKTDDLDADGKRPIEKAVLWKKLKAVKNGHVYHVDR 320
                                                                                                                                                              127
                                                                                                                                                                                             187
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                                           68
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                                                                                                                                                                                                                                                                                                                TTRHKKVYDQLKKIAPTIALNNINADYQDTIDASLTIAKAVGKEKEMEKKITAHBEKLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                      205 TKQKISAN-SQSVLLIGNTNDTIMARDENFFTSRLLTQVGYRYAIS---TSGNSDSSNGG
                                           KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                          VDALVALDVKPVGIADDNKKNRII-KPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                                 NNRHKGI YKDLNKI APTI ELKSFDGDYNEN I DAFKTI SKALGKEBEGKKRLEEHDKKI BE
                                                                                                                                                                                                                                                                                                                                                                                                          YKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSOLGFKEALSDDVTKGLSKYLKG-
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A;Start codon: GTG
C;Superfamily: ferrichrome-iron transport protein fecB
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12;

67 62

Length 341;

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A;Residues: 1-341 <GTO>
A;Cross-references: UNIPROT:Q9KE21; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
A;Cross-references: UNIPROT:Q9KE21; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
B;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1037
A; Reference number: A83650; MUID: 20512582; PMID: 11058132
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Pred. No. 8.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                  29.7%;
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33.0%;
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Matches 102; Conservative
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Best Local Similarity
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                                          A; Accession: E83779
A; Status: preliminary
A; Molecule type: DNA
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C;Species: Bacillus aubtilis

R;Kunst. F.; Ogsawara, N.; Macser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chanser, E.; Bron, S.; Bruschi, C.Y.; Entian, K.D.; Errington, J.; Pabret, C.; Fruita, M.; Fulita, Y.; Fuma, S.; Galizzi, A.; Galler

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Kuita, K.; Lapidus, A.; Ital, M.; Macuda, S.; Maued

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Macuda, S.; Maued

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Macuda, S.; Maued

A;Authors: Collect, S.; Schroeter, F.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scollon,

A;Authors: Schleich, S.; Schroeter, H.; Yashano, K.; Yashanoto, V.; Granlon,

A;Authors: Schleich, S.; Schroeter, H.; Yashanoto, K.; Yashanoto, V.; Uchiyama,

T.; Winters: P.; Mipat, A.; Tamaka, H.; Danchin, A.; Tamakoshi, A.; Secondon,

A;Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tamakoshi, A.; Secondon,

A;Actrae: preliminary; nucleic acid sequence not shown; translation not shown

A;Mclecule type: DNA

A;Restence number: A59580; MUID:98044033; PMID:9344377

A;Restence number: A59580; MUID:98044033; PMID:9344377

A;Restence strain 168

C;Gene: Strain source: strain 168

C;Gene: Yfill

A;Gene: Yfill

A;Gene: Yfill

C;Superfamily: iron(III) dicitrate transport protein
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29.8%; Pred. No. 4.5e-14;
tive 75; Mismatches 129; Indels
        289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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Best Local Similarity
Matches 96; Conserv
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probable ferrichrome ABC transporter yclQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: E69763
B;Runet, F:) Ggasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V:; Berter.
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B:; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujitz, M.; Fujitz, X.; Fumer, S.; Galizzi, A.; Galler, i. Henauch, S.; Kunano, M.; Kunita, K.; Lapidus, A.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kunano, M.; Kunita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, W.; Ogdwa, K.; Oddega, B.; Park, S.H.; Parro, V.; Poll, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlo,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sckowska, A.; Serox
acuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, M.; A;Atterence number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69763
A;Accession: E69763
A;Accession: E69763
A;Accession: preliminary; nucleic acid sequence not shown, translation not shown
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
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                                                                                                                                                                                                                                                                   65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 FLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKEL
                                                                                                                                                                                11 LSVIGLLFVLIATAACGNNSSSNSS-----KESSKDGVE-----IKHEEGTTKV
                                                                                                                                                                                                                                                                                                                                                           55 PKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLE
                                                                                        40;
i Score 350; DB 2; Length 34
j Pred. No. 9.4e-13;
63; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 EKDPVWKKINAVKNORVDILDRDLWARSRGLISSEEMAKELVE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: yclQ
C;Superfamily: iron(III) dicitrate transport protein
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Length 317;

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iron(III) dicttrate-binding periplasmic protein [imported] - Nostoc sp. (strain PCC 7120 c)5pecies: Nostoc sp. PCC 7120 sp. strain PCC 7120 c)5pecies: Nostoc sp. errain PCC 7120 c)70te: Nostoc sp. strain PCC 7120 c)5pecies: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 c)5Accession: AR12128 c)5Accession: AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 «KUR»
A;Cross-references: UNIPROT:Q8YTX0; GB:BA000019; PIDN:BAB74282.1; PID:g17131675; GSPDB:C
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ironical dicitrate-binding periplasmic protein of ABC transporter alr2213 [imported] - ironical better Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession AG2082
R,Xaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigucha Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. Nakamura, Shimpo S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. Nakamura, Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy, Recession: AG2082
A,Recession: AG2082
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A;Residues: 1-325 «KUR»
A;Cross-references: UNIPROT:Q8YUW8; GB:BA000019; PIDN:BAB73912.1; PID:g17131304; GSPDB:C
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : :| |::||||: | | | |: | | | |: |: || |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 FVDALVALDVKPVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
19.3%; Score 327; DB 2; Length 328;
Best Local Similarity 29.8%; Pred. No. 1.7e-11;
Matches 97; Conservative 71; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: alr2583
C;Superfamily: ferrichrome-iron transport protein fecB
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C; Genetics:
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Ol-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G84123
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Recession: G84123
A;Recession: G84123
A;Recession: G84123
A;Residuss: 1-314 <5TO)
A;Cross-references: UNIPROT:Q9K6D8; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB075
C;Genetics:
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                                                                                                                                                                                                                                                                                         IEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOF--LSQLG----FKEALSDDVT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 IADVKK--TAEK------LNKNGLVIMANDGKISAFGPKSRYGLIHDVFGVAPADQNI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNE-PSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                        DNNRHKGIYKDLNKIAPTIELKSPDGDYNENI--DAPKTISKALGKEEEGKKRLEEHDKK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 KASTHGGSVSY----EYISKTNPDYLFVIDRGTAIGETSSTKQVVENDYVRAVKANG
                                                                                LLFVLIATA----ACGNNSSSNSSKESSKDGVEIKH--EEGTTKVPKHPKRVVVLEYSFV
                                                                                                                                                                                                                                          DAL -- VALDVKPVGIADDNKKNRIIKPL-RDKIGKYTSVGTRKOPNLEEISKLKPDLIIA
    Gaps
    41;
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59; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVDILDRDLWARS-RGLISSEEMAKEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 HVIYLDSATWYLSGGGLESMTOMIKEV 311
    108; Conservative
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        Matches
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iron(III) dicitrate-binding periplasmic protein fecB-2a - Synechocystis sp. (strain PCC NyAlternate names: protein s1r1491 (5.Species: Synechocystis sp. (5.Species: Synechocystis sp. A;Variety: PCC 6803 (5.Species: Synechocystis sp. A;Variety: PCC 6803 (5.Species: 25-Apr-1997 #text_change 09-Jul-2004 (5.Species: 25-Apr-1997 #text_change 09-Jul-2004 (5.Species: 574458 (5.Species: Synechos: S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996 (5.Species: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-330 <KAN>
A;Cross-references: UNIPROT: P72610; EMBL: D90899; GB: AB001339; NID: g1651650; PIDN: BAA1661
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Accession: S74458
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                         292 SISAHNTNRIYFIDYQLASRIRGPIAABLFVNQVRQL 328
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llarity 28.4%; Pred. No. 1.5e-09;
Conservative 68; Mismatches 119;
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A;Gene: fecB 2a
C;Superfamily: iron(III) dicitrate transport protein
C;Superfamily: 092 5; DB 2
                                                                            289 KINAVKNORVDILDRDLWARSRGLISSEEMAKELVEL
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243 K-LVSPESTE-
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-319 <KUR>
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A; Reference number: AB1807; MUD:21595285; PMID:11759840
A; Recession: AG3129
A; Restous: preliminary
A; Molecule type: DNA
A; Residues: 1-330 cKUR>
A; Residues: 1-330 cKUR>
A; Residues: 1-330 cKUR>
A; Reperimental source: strain PCC 7120
C; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                       DLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENI--DAFKTISKALGKEEEGKKRLE 179
                                                                                                                                                                                                                                                                                                                                                                                     EHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDV--- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 ----TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                      62 VVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLBEISKLKP 121
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                                                                                                                                                        6 RGLKILSVIGLLFVLIATAACGNNSSSNS----SKESSKDGVEIKHEEGTTKVPKHPKRV
                                                                                                                                                                                                      7 RYIKLFILIPLTLVLV--NSCYINYPENSGLITTRIKTSECRLIKHPLGESCVPVKPORV
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                                                     ch 18.3%; Score 310; DB 2; Length 325; 1 Similarity 28.3%; Pred. No. 1.6e-10; 89; Conservative 71; Mismatches 124; Indels
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            C, Superfamily: ferrichrome-iron transport protein fecB
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184 KIEEYKKEITM-DKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDV----
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Matches 85; Conserv
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C; Species: Nostco sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostco sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Accession: AF2082
C; Accession: AF2082
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpoo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res B, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Residues: 1-326 <KUR>
A; Molecule type: DNA
A; Residues: 1-326 <KUR>
A; Cross-references: UNIPROT:Q8VUW9; GB:BA000019; PIDN:BAB73911.1; PID:g17131303; GSPDB:C
C; Genetics:
C; Genetics:
A; Gene: alr2212
C; Superfamily: ferrichrome-iron transport protein fecB
A,Cross-references: UNIPROT:Q8YML0, GB:BA000019; PIDN:BAB76622.1; PID:g17134061, GSPDB:GA; Experimental source: strain PCC 7120
Genetics:
A;Gene: a114923
C;Superfamily: ferrichrome-iron transport protein fecB
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                                                                                                                                                                                                                                                                                                                                                      LSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 EYSFVDALVALDVKPVGIADDNKKNRIIKPL-RDKIGKYTSVGTRKQPNLEEISKLKPDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 IIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 SKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDG--DYNENIDAFKTISKALGKEEEG 174
                                                                                                                                                                                                                                                                                                                                                                                                           KKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSN---SYVGQFLSQLGFKEA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 IKLLLVITLIIVFFKGCHSFLTQNIYSSNEYVKSTECRI-IKHKLGEICIPLNPQRIIVT 68
                                                                                                                                                                                                                       55
                                                                                                                                                                                                          MRNSKPLLFLLTIVVVLALAACNHN-----IPQSAKSQIATRIVSNTLGEVKVPLKPQRV
                                                                                                                                                                                                                                                                                          56 VVLEENIVLDSVLALGIKPVGVAYCRECEEKFRGIPSDLLADVPVVGNIGT--QPSLEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                8 LKILSVIGLLFVLIA---TAACGNNSSSNSSKESSKDGVEIXHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                     5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGV---EIKHEEGTTKVPKHPKRV
                                                                                                                                                   Gaps
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                                                                                                                                                   Indels 37;
                                                                                                                 Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.0%; Score 288; DB 2; Length 32 Best Local Similarity 26.2%; Pred. No. 2.7e-09; Matches 87; Conservative 78; Mismatches 137; Indels
                                                                                                               ch 17.1%; Score 288.5; DB 2;
1 Similarity 29.9%; Pred. No. 2.5e-09;
93; Conservative 66; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKLNAVKNORV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 SKLKAVQNKQV 291
                                                                                                                                                                                                                                                               62
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                                                                                                                 Query Match
Best Local S
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periplasmic iron-compound-binding protein of iron(III) ABC transporter all0388 [imported periplasmic iron-compound-binding protein of iron(III) ABC transporter all0388 [imported C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession: AC1855
R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res 8, 205-213, 2001
A,Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A,Accession: AC1855
A,Status: preliminary
A,Residues: 1-300 <KURN.
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A,Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SA0691 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89846
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                    236
                                                                                                                         VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEBISKLKPDLIIADNNRHK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GIYKDINKIAPTIELKSFDGDYNEN-ID----AFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQTAATRIKNTQKPDFVLGQFSDNAPQIRLFTDNSMATQILTAIGLKNA------
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18 FVLIATA----ACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                      237 -TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%; Score 285; DB 2; Length 300; 26.0%; Pred. No. 3.6e-09; ive 64; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: al10388
C;Superfamily: ferrichrome-iron transport protein fhuD
                                                                                                                                                                                                                                                             295 NHVYTVDSGYWIFGNILSANAILDDIVKYLVE 326
                                                                                                                                                                                                                          QRVDILDRDLWARSRGLISS---BEMAKELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDILDRDLWARSRGLISSEEMAKELVE 324
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iron(III) dicitrate-binding periplasmic protein of ABC transporter alr2210 [imported] - G.Species: Nostco sp. PCC 7120
G.Species: Nostco sp. pCC 7120
G.Pacession: Nostco sp. ercain PCC 7120
G.Pacession: AD2082
G.Pacession: AD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:QBYUX1; GB:BA000019; PIDN:BAB73909.1; PID:gl7131301; GSPDB:GA;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                242
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                                                                                                                                                         187 QKMG-NKLSKIKVSV----VRVYPDKINLYLLDSFCGTILQDAGLSRPESQNFTASEAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 ALVALDVKPVGIADDNKKORIIKPLRDKIGKYTSVGTRKOPNLBEISKLKPDLIIADNNR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPYLOMNTETL-SOVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 IALGIKPLGAVISDFSSF-----WKDKLTGVKNIGTTGEPNLESILALKPDLIVG-SDY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
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                                                                                                           131 HKGIYKDLNKIAPTIELK-SFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYK
                                                                                                                                                                                                                                                                    190 KEITMDKNQKVLPAVAAKSGLLAHPS-----NSYVGQFLSQLGFKEALSDDVŢKGLSK
                                                                                                                                                                                                                                                                                                                                                                                                                             243 YLKGPYLQM--NTETLSQVNPERMFIMT--NKASSNEPS---LKELEKDPVWKKLINAVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKGIYKDLNKIAPTIELKSPDG--DYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEY
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16.5%; Score 279.5; DB 2;
Best Local Similarity 25.8%; Pred. No. 8.2e-09;
Matches 82; Conservative 75; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: alr2210
C,Superfamily: ferrichrome-iron transport protein fecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 NKVYVVP-SYWIGS-GMLAANAIIDDL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 QRVDILDRDLWARSRGLISSEEMAKEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWARSRGLISSEEMAKEL 322
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AE2074
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A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Residues: preliminary
A; Status: preliminary
A; Residues: 1-331 - KNR>
A; Residues: 1-332 - KNR>
A; Residues: 1-332 - KNR>
A; Reperimental source: strain PCC 7120 C; Genetics: A; Genetics: Genetics: A; Gen
                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q99VN8; GB:BA000018; PID:g13700627; PIDN:BAB41924.1; GSPDB:G
C;Genetics:
A;Gene: SA0691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 ---TISKALGKEEBGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAH-PSNSY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 VPKHPKRVVVLEYSFVDALVALDV-KPVGIADDNK---KNRIIKPLRD-----KIGKYTS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGTRKOPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFK- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 VGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 GGLVYDTLGF----NAVDKKVSNSNHGQ--NVSNEYVNKENPDVILAMDRGQAISGKST 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VIGLLFVLIATAACGNNSSSNSSKESS------KDGVEIKHEEGTTK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                              Stapylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 VLAVMPLL --- AACGNNSDKEQSKSETKGSKDTVKIENNYKMRGEKKDGSDAKKVKETVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 IGLLFVLIATAACGNNSSSNSSKESSKDGV-EIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 AKQALNNPVLKNVKAIKEDKVYNLDPKLMYPAAG--STTTTIKQIEELDK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
16.9%; Score 285; DB 2; Length 342
Best Local Similarity 28.9%; Pred. No. 4.2e-09;
Matches 101; Conservative 61; Mismatches 134; Indels
Lancet 357, 1225-1240, 2001
Affile: Whole genome sequencing of meticillin-resistant: A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: A89846
A/Status preliminary
A/Residues: Draliminary
A/Residues: 1-342 <KUR>
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Best Local Si
Matches 92;
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A, Residues: 1-357 < KUR>
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                                                                                                                                 P. Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

DNA Res. 8, 205-213, 2001

A. Tatitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A. Reference number: AB1807; MUID:2159285; PMID:11759840

A. Reference number: AB1807; MUID:2159285; PMID:11759840

A. Status: preliminary
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AD2085
A;Status preliminary
A;Accession: Nnn
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A;Molecule type: DNA
A;Residues: 1-119 <KUN>
A;Experimental source: UNIPROT: Q8YUU6; GB:BA000019; PIDN:BAB73934.1; PID:g17131326; GSPDB:
A;Experimental source: strain PCC 7120
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C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2074
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDG--DYNENIDAFKTISKALGKEBEGKK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 LRLIQQNQKQRELTLSIEVLPKYDADILFIMTEHLTRDFKEANPEVLSFLQK-PIWSNLK 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 TKGLSKYLKGPYLOMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVWKKLN 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVE----IKHEEGTTKVPKHPKRVV
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16.4%; Score 278; DB 2; Length 361;
Best Local Similarity 29.3%; Pred. No. 1.1e-08;
Matches 90; Conservative 63; Mismatches 124; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 319;
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Best Local Similarity 25.1%; Pred. No. 1e-08;
Matches 82; Conservative 72; Mismatches 138;
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AVKTKQI 333
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C;Species: Nostco sp. PCC 7120
A;Note: Nostco sp. PCC 7120
A;Note: Nostco sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2079
R;Kanako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anc. A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8YUZ5; GB:BA000019; PIDN:BAB73885.1; PID:g17131277; GSPDB:<A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iron(III) dicitrate-binding protein of ABC transporter alr2186 [imported] - Nostoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGKEEEGKKRLEEHDKKIEEYKKEIT--MDKNQKVLPAVAAKSGL---LAHP-SNSYVGQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ALGLKPMGAPDTTYVASKSSFLKSKMSGINYIGKEDQFNLEKILNLHPDLIISLYGINSA 130
                                                                                                                                                                                                                                                                                                                                                               247
                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YLQMNTETLSQVNPERMFIMTNKASSNEPSLKEL----EKDPVWKKLNAVKNQRVDI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 PKRVVVLEYSFVDALVALDVKPVGIAD------DNKKORIIKPLRDKI-GKYTSVGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 IYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEIT 193
                                                                                                                                                                                                                                                                           --EPSLKELE----KDPVWKKINAVKNQRVDILDRDLWARSRGLISSE----EMAKELV 323
                                                                                                                   ALDVKPVGIADDNKKORIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKG 133
                                  222 FLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSN-----
                                                                                                                                                                                                                                                                                                                                                                                              188 NQTNQLKVSVSRFHGGV-----QLPEFRSQFSFPGSILQEV--GISMPNAQRQLIKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VRGLKILSVIGLLFVLIATA----ACGNNSSSNSSKESSKDGVE---IKHEEGTTKVPKH
                                                                                                                                                                                                                                                                                                                                                            194 MDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLS-----KYLKGP
LFVLIATAACGNNSSSNSSKESSKDGVE---IKHEEGTTKVPKHPKRVVVLEYSFVDALV
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16.4%; Score 277.5; DB 2; Length 357;
Best Local Similarity 27.3%; Pred. No. 1.2e-08;
Matches 98; Conservative 76; Mismatches 134; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | : : | 1 | 293 VDSSYWIFG-SILSANAIVDDLFKYLK 318
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KGP-YLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ALDVKPVGIADDNKKNRIIKPLR---DKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GADI-KKLEKIAPTVAVKY---DKLDNIEQLKEFAKMTGTEDKAEKWLAKWDKKVAAAK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFVLIATAACGNNSSSNSSKESSKDGVE---IKHBEGTTKVPKHPKRVVVLEYSFVDALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 315,
                                                                      N.Alternate names: ferrichrome-binding protein fhuD
C;Species: Bacillue enhall:
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// Pred. No. 1.4e-08;
42; Mismatches 121; Indels
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Best Local Similarity 32.1*
Matches 97; Conservative
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Cippedies: Bacillus subtilis
Cipter: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
Cipter: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
Cipter: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
Richis. Biophys. Acta 1186, 27-34, 1994
Airtie: Isolation of They? Insertional mutants of Bacillus subtilis that are resistant
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Airtie: Isolated from GB/BMBL/DDBJ
Airtie: Isolated from GB/BMBL/DDBJ
Airtie: Isolated from GB/BMBL/DDBJ
Airticas-references: UNIPPO: PACAPA; Airtie A., Isolate, C.; Febrari, E.
Airticas-references: UNIPPO: PACAPA; Airtie A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A.; Isolate, A
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294 YFEPQMQKLKQQWSENAIAQSLTASKEGRVYFIPAYLCLGLPGPIGTELYLQELQKQLL 352
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Best Local Similarity 26.5%;
Matches 86; Conservative
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iron(III) dicitrate-binding periplasmic protein [imported] - Nostoc sp. (strain PCC 7126 C; Species: Nostoc sp. PCC 7120 A; Note: Nostoc sp. pcC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C; Accession: AB2130
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A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A; Reference number: AB1807; MUID:21595285; PMID:11759840

A; Accession: AB2130

A; Status: preliminary

A; Molecule type: DNA
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A,Cross-references: UNIPROT:Q8YTX0; GB:BA000019; PIDN:BAB74292.1; PID:g17131686; GSPDB:
A,Experimental source: strain PCC 7120
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126 KPDLILGLAESTDRKS-YELPSQIAPTVTV----DYAQTAWRDVLLRVGNIIGKTEQAQ 179
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                               8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVE---IKHEEGTTKVPKHPKRVVV
-VEIKHEEGTTKVPKHPKRVVVL
                                                                                                 EYSFVDALVALDVKPVGIADDNKKNRIIKP------LRDKIGKYTSVGTRKQ----PN
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16.2%; Score 273; DB 2; Length 333;
Best Local Similarity 28.3%; Pred. No. 1.9e-08;
Matches 90; Conservative 65; Mismatches 127; Indels
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C;Superfamily: ferrichrome-iron transport protein fecB
  14 IGLLFVLIATAACGNNSSSNSSKESSKDG-
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          iron([II) dicitrate-binding periplasmic protein of ABC transporter al12157 [imported] -
[iron(III) dicitrate-binding periplasmic protein of ABC transporter al12157 [imported] -
[ispecies: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AG2075

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res 8, 205-213, 2001

A;Reference number: AB1807; MUD:21595285; PMID:11759840

A;Reference number: AB1807; MUD:21595285; PMID:11759840

A;Recession: AG2075

A;Retus: preliminary

A;Molecule type: DNA

A;Recessidues: 1-343 < KUR>
A;Recessidues: 1-343 < KUR>
A;Recessidues: UNIPROT:Q8YV24; GB:BA000019; PIDN:BAB73856.1; PID:g17131248; GSPDB:C

C;Genetics:
A;Experimental source: strain PCC 7120

C;Genetics:
A;Antanary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GILHDIGILNPIFAE-----SGDYDLPLSEELLPNIDSDILFIAPLR-KDDYSVIK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 PLKPQRIVTLDFNSFAALLALDTKPIATWITTEIEDDFPYFQGKAEGVEILRSSSG---- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 QFLSQLGFKEALSDDVTKGLSKYLKGPY-LQMNTETLSQVNPERMFIMTNKASSNEPSLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKHPKRVVVLEYSFVDALVALDVKPVG-----IADD----NKKNRIIKPLRDKIGKYTS 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 RGLKILS----VIGLLFVLIATAACGNNSS-----SNSSKESSKDGVEIKHEEGTTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.2%; Score 274; DB 2; Length 343;
Best Local Similarity 26.5%; Pred. No. 1.8e-08;
Matches 91; Conservative 80; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 KLQQKPLWSKLKAVQQNQVYIVDFSVW-RGLNMLAAYAMLDDL 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: ferrichrome-iron transport protein fecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: all2157
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ferrichrome binding protein homolog lmo1959 [imported] - Listeria monocytogenes (strain FG, Species: Listeria monocytogenes (classe: Listeria monocytogenes (classe: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (classer, P.) Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker; Dominguez-Bernal, G.; Duchaud; E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 (classer, B.) Ashuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mathors: Kreft, J.; Kuhn, M.; Tarerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Accession: Agills MulD:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - - - - - DEVASLGANVVGTDSWAPPNTFLSKDQKKNMV------DLGAPKF-NMEKLIA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 LKPDLIIADNNRHKGIYKDLNKIAPT--IELKSFDGDYNENIDAFKTISKALGKEEBGKK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 QNPDLIITVD----AKLLANREDEKAS 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 PKEALS-DDVTKGLSKYLKGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPV 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOP-NLEEISKLKPDL 123
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                                                                                                                                                                                                                                         9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                                                                                                                                                                                                                                                                                          3 KVLTTLIAAGALLTLAACSSNSSSKKA-TSSDDKVTFHALNGDVKVPKNPKRIAVQNYP-
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C;Superfamily: Bacillus subtilis ferrichrome ABC transporter fhuD
                                Length 313;
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; Pred. No. 5.4e-08;
68; Mismatches 114; Indels

    Score 265; DB 2; Length 31
    Pred. No. 5e-08;
    Mismatches 116; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 WONLKAVKEGHVITMDYD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Experimental source: strain EGD-e
C, Genetics:
                     15.7%;
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                                Query Match
Best Local Similarity 29.2%
Matches 93; Conservative
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                                                                                                                                                                                                                                         iron(III) dicitrate-binding periplasmic protein [imported] - Nostoc sp. (strain PCC 7120 C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. PCC 7120 A;Note: Nostoc sp. pCC 7120 A;Note: Nostoc sp. strain PCC 7120 C;Species: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: A11943 R;Kaneko. T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, A.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11943 A;Accession: A11944 A;Accession: A11944 A;Accession: A11943 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accession: A11944 A;Accessio
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A,Experimental source: strain PCC 7120
A;Genteins: A:Constant Source: strain PCC 7120
A;Gente: all:100
C;Superfamily: ferrichrome-iron transport protein fecB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SYVGQFLSQLGF 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNNRHKGIYKDLNKIAPTIELKSFDGDYNEN--IDAFKTISKALGKEEGKKRLEEHDKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LLFVLIATAAC----GNNSSSNSSKESSKDGVEIKHEEGTIKVPKHPKRVVVLEYSFVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 267.5; DB 2; 26.1%; Pred. No. 3.9e-08; tive 61; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLNAVKNORVDILDRDLW 306
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KLKAVKNNCVYTVDSGYW
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Campylobacter jejuni

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enterochelin uptake periplasmic binding protein Cj1355 [imported]
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                                                                                                                                                                                                                                                                                                             ABG transporter (binding protein) homolog yxeB - Bacillus subtilis
C;Species Bacillus subtilis
C;Species Bacillus subtilis
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C;Species Bacillus subtilis
C;Species Bacillus subtilis
C;Accession: D70074
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C;Brunch, S.D; Emmerson, N.; Moracle, D; Fritz, C; Fulita, M.; Fulita, M.; Fulita, C; Ferrari, E.
Nature 390, A49-256, 1997
A,Authors: Poulger, D; Fritz, C; Fulita, M.; Fulita, K.; Funa, S.; Galizzi, A.; Galler
A,Authors: Poulger, D; Fritz, C; Fulita, M.; Fulita, K.; Liu, H.; Masuda, S.; Maucel
A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekfyuchi, J.; Schowska, A.; Secondan, A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekfyuchi, J.; Schowska, A.; Secondan, A,Muthors: Schleich, S.; Sumancto, H.; Yeshikawa, H.; Danchin, A.; Tosato, V.; Uchiyana, T.; Minters, P.; Wipat, A.; Yamamoto, H.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, M.; Maccession: D70074
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Boccesion: D70074
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Boccesion: D70074
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Boccesion: D70074
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Boccesion: UNIPROT.P54941; GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CABIS997.
A,Gene: Tyces
C;Generices: Strain 168
C;Generices: Strain 168
C;Generices: Strain 168
C;Generices: Strain 168
C;Gene
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                                                              EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQP-NLEBISKLKPDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 IIADNNRHKGIYKDLNKIAPTIELKSFDGDYN--ENI-DAFKTISKALGKEEEGKKRLEE 180
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27.2%; Pred. No. 8.1e-08;
tive 55; Mismatches 123;
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                                                                                                                                          LNAVKNORVDILDRD 304
                                                                                                                                                                              274 LPTFKAGNVYQMDFD 288
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Best Local Similarity 27.2%;
Matches 87; Conservative
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RESULT 33 H81279

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Cispecies: Campylobacter jejuni
Cispecies: Campylobacter jejuni
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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Car,; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf.
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-330 <PAR>
A; Cross-references: UNIPROT: Q9PWU4; GB:AL139078; GB:AL111168; NID: G6968723; PIDN: CAB7376
A; Experimental source: serotype O2, strain NCTC 11168
C; Genetics:
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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A;Cross-references: UNIPROT:P72593; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA165:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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73 VVILDLGILDTFDALKINDKVVGVPAKNLP-KYLQQFKNK----PSVGGVQQVDFBAINA 127
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A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 330;
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15.4%; Score 261; DB 2; Length 33
Best Local Similarity 26.3%; Pred. No. 9e-08;
Matches 88; Conservative 72; Mismatches 123; Indels
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C,Superfamily: iron(III) dicitrate transport protein
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hypothetical protein ABC-SBP [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F97988
C;Accession: F97988
C;Accession: FP, is Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. F; Hosking, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; WUID:21429245; PMID:11544234
A;Reference number: Apyrelminary
A;Accession: F97988
A;Status: preliminary
A;Accession: F97988
A;Accession: F97988
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A;Residues: 1-341 <KUR>
A;Cross-references: UNIPROT:Q97R09; UNIPROT:Q8DPY6; GB:AE007317; PIDN:AAK99738.1; PID:g1
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S;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
S;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
S;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
S;Racession: AFD130
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sl
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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                                                                                        284 ALQKDPLLGKINAIKNGAVAVI 305
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                                         ELEKDPVWKKLNAVKNORVDIL
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Best Local Similarity 28.9%
Matches 93; Conservative
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C,Genetics:
A,Gene: ABC-SBP
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C; Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Accession: B5519
R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: A5000; MUID:21357209; PMID:11463916
A; Reference number: A55000; MUID:21357209; PMID:11463916
A; Residues: Preliminary
A; Molecule type: DNA
A; Residues: 1-341 *KUR.
A; Residues: 1-341 *KUR.
A; Cross-references: UNIPROT:Q9DR09; UNIPROT:Q8DPY6; GB:AE005672; PIDN:AAK75147.1; PID:gl
C; Ganetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLSQLG--FKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLK 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 ELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 YFIYIGDSGDQTPGSITNPWLNHPLWQQLEVVQSGKAYAVSDVVWTTAGGIQAAHLLLDD 308
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                                                                                                                                                                                         28 GETIQSNLTQRT-----IAHAMGVTAVPNEPQRIVVLTNEATDMVLALGVTPVGAVKSW
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                                                                                                                             27 GNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 AKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERM-
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                                         Indels
Pred. No. 9.6e-08;
64; Mismatches 136;
25.6%;
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Matches 93; Conservative
                                         77; Conservative
Similarity
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Matches 7
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E90802
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; P. R;Hoskins, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; S. P.; Sun, P.M.; Winkler, M.E.
Y, P.; Sun, P.M.; Winkler, M.E.
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R., A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-321 «KUR»
A;Gross-references: UNIPROT:Q8DNJ2; GB:AE007317; PIDN:AAL00490.1; PID:g15459362; GSPDB:<
C;Genetics:
                                                                                              236
                                                                                                                                                                                        236
                                                                                                                                                                                                                                                                                       TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                 284
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                                                                                                                                                                                                                                                                                                                                         20 LIATAACGNNSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV
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                                                                                                                                                          187 VATKNESSDKKALAILLINBGKMAAFGAKSRF-----SFLYQTLKFKPTDTKFEDS
                                                                                              --KKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQ-LGFK--BALSDDV
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26.8%; Pred. No. 2.4e-07;
ive 66; Mismatches 117; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
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A;Molecule type: DNA
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Matches 91; Conserv
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96; Conserv
              A;Experimental source:
C;Genetics:
A;Gene: alr2597
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: D83778
A;Accession: D83778
A;Actus: D84
A;Residues: 1-329 <STO>
A;Cross-references: UNIPROT:09KE30; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
A;Cross-references: strain C-125
C;Genetics:
A;Gene: BH1028
                                                                                                                                                                                                                                                                                                                                                                                                 113 LEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNEN-IDAFK----TISKA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 FETIYDLQPDLIII-SGRTSEAYDELSDIAPTL---FVGLDTENYLESFRSNMETLGEI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 FGKETEVBEALASLEASIEEV-QQLAAEKEETGLIVLANDGNVSAYGPGSRFGVIHDEFG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 V----TPVDENIEVSNHGQ--SISFEYIVEKNPDHLFVIDRGAVVQEGEETNIENELV- 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 LGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 FKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW 287
                                                                                                                                                                                                                                                                                                                                              10 ILSVIGLLFVLIATAACGNNSSSN----SSKESSKDGVE------IKHEEGTT 52
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                   DB 2; Length 329;
                                                                                                                                                                                                                                   Query Match
14.8%; Score 250.5; DB 2; Length :
Best Local Similarity 25.6%; Pred. No. 3.5e-07;
Matches 86; Conservative 71; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 QQTTAYEEGNIHYLTPDYWYISGGGLVSVEQMIDEM 324
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Search completed: August 25, 2005, 09:27:10 Job time : 24 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

August 25, 2005, 09:27:00 ; Search time 163 Seconds Run on:

(without alignments) 807.548 Million cell updates/sec

US-10-724-972A-6352 1690 Perfect score:

1 GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK 335 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1767149 seqs, 392926209 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
 /cgn2 6/ptodata/2/pubpaa/BCT NEW PUB.pep:*
 /cgn2 6/ptodata/2/pubpaa/BCO NEW PUB.pep:*
 /cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
 /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
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Cgn2 6/ptodata/2/pubpaa/US10D_PUBCOMB.pep. /cgn2 6/ptodata/2/pubpaa/US10E_PUBCOMB.pep. /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep. /cgn2 6/ptodata/2/pubpaa/US11A_PUBCOMB.pep. /cgn2 6/ptodata/2/pubpaa/US11MEW PUB.pep. /cgn2 6/ptodata/2/pubpaa/US11MEW PUB.pep. /cgn2 6/ptodata/2/pubpaa/US11MEW PUB.pep.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6352, Ap	Sequence 71138, A	Sequence 12254, A	Sequence 43828, A	Sequence 5459, Ap	Sequence 5249, Ap	Sequence 12122, A	Sequence 44133, A	Sequence 329, App	Sequence 71291, A	Sequence 66890, A
		335 18 US-10-724-972A-6352	US-10-282-122A-71138	US-09-815-242-12254					15 US-10-282-122A-41133			
	BB	18	15	0	15	σ	δ	σ	15	1.7	15	15
	Query Match Length DB ID	335	331	337	327	309	319	319	319	319	175	298
Þ	Query	100.0	98.7	73.5	72.9	6.69	43.0	43.0	42.9			
	Score	1690	1668	1242	1232	1181	726	726	724.5	724.5	£44	516.5
	Result No.	1	8	٣	4	S	9	7	6 0	σ	10	11

Sequence 56054, A	Sequence 10469, A	Sequence 56805, A	Seguence 69420, A	193,	16, A	2	34	Sequence 16, Appl	Sequence 45599, A	Sequence 3875, Ap	Sequence 53267, A			Sequence 46193, A	Sequence 7181, Ap	878	ະ	Sequence 38, Appl	Sequence 38, Appl	Sequence 10905, A	Sequence 46179, A	Sequence 40, Appl	Sequence 40, Appl	Sequence 40, Appl	4	ഗ	4731	663,		2046	ř	o,	Sequence 3884, Ap
15 US-10-282-122A-56054	9 US-09-815-242-10469	5 US-10-282-122A-568	-122A-69					17 US-10-967-189-16	15 US-10-282-122A-45599	9 US-09-738-626-3875	15 US-10-282-122A-53267	15 US-10-282-122A-46283	15 US-10-282-122A-45385	15 US-10-282-122A-46193	18 US-10-724-972A-7181	15 US-10-282-122A-68785	9 US-09-071-035-38	US-10-206-576	17 US-10-912-362-38	9 US-09-815-242-10905	15 US-10-282-122A-46179	9 US-09-071-035-40	14 US-10-206-576-40	17 US-10-912-362-40				16 US-10-474-776-663			9 US-09-815-242-13454	US-10-415	17 US-10-472-928-3884
300	302	302	297	330						315							317	317	317	317	315	296	296	296	306	306	342	341	341	341	321	321	321
27.2	27.2	27.2	26.9	24.0	24.0	24.0	24.0	24.0	23.1	19.6	19.3	18.5	17.8	17.8	17.5	17.5	16.7	16.7	16.7	16.5	16.2	15.9	15.9	15.9	15.7	15.7	15.2	15.0	15.0	15.0	15.0	15.0	15.0
460	460	460	454	405	405	405	405	405	391	331	327	313	301	300	296.5	296	283	283	283	279	274.5	268	268	268	266	266	257.5	254	254	254	253	253	253
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

AL IGNMENTS

APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
TITLE OF INVENTION: WICKEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 1099-11-01
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR PILING DATE: 1999-10-3
PRIOR FILING DATE: 1999-10-4
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544 Sequence 6352, Application US/10724972A Publication No. US20040147734A1 GENERAL INFORMATION: ; ORGANISM: S.epidermidis US-10-724-972A-6352 US-10-724-972A-6352

Gaps ö Length 335; 0; Indels Score 1690; DB 18 100.0%; Scor. 100.0%; Pred. No. o. o. Mismatches Query Match Best Local Similarity 100. Matches 335; Conservative

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Gaps

244

304

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241 KGPYLQMNTETLSQVNPERMFIMTNKASSNBPSLKELEKDPVWKKLNAVKNQRVDILDRD 300
                                                                                                                                                                                                                                                         65 EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLI 124
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                                                                                                                                                    61 EYSFVDALVALDVKFVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                  125 IADNNRHKGIYKDLNKIAPTIELKSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGPYLOMYTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD
                                                                                                         5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 IBEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSOLGFKEALSDDVTKGLSKYL
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   99.7%; Pred. No. 2.1e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 LWARSRGLISSEEMAKELVELSKKDSKKDNK 331
                                   1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12254, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus aureus
US-09-815-242-12254
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Best Local Similarity 72.0*
Matches 236, Conservative
Best Local Similarity 99.7
Matches 330; Conservative
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                                              VVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLK 120
                                                                                     61 VVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                  181 HDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGL 240
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APPLICANT: Wall, Daniel
APPLICANT: Trawlick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Porsyth, R.
APPLICANT: W. H.
APPLICANT: W. H.
APPLICANT: W. H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                           HDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDVTKGL
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2001-02-3
PRIOR FILING DATE: 2001-02-3
PRIOR FILING DATE: 2001-02-3
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 71138, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Staphylococcus epidermidis US-10-282-122A-71138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Amnio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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125 IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKK 184
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                                                                                                                                                                       5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                          Length 327;
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APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Kanamotc, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/203.21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
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; Pred. No. 2.5e-72;
38; Mismatches 46;
                       ; Score 1232; DB 15;
; Pred. No. 9.1e-76;
42; Mismatches 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5459, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5459
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ilarity 71.9%;
Conservative 45
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Best Local Similarity 72.8
Matches 225; Conservative
                             Query Match
Best Local Similarity
Matches 235; Conserv
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                                                                                                                                                                                                                                  184 KIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKY 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDR 303
                                69
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-06
PRIOR PLILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-16
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PRIOR PLILING DATE: 2001-02-16
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PRIOR PLILING DATE: 2001-02-16
PRIOR PLILING DATE: 2001-02-16
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLWARSRGLISSEEMAKELVELSKKDSK 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Staphylococcus aureus US-10-282-122A-43828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Forsyth, R.
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Trawick, John
Carr, Grant
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59 YSFADYLAALDMKPVGIADDGSSKNITKSVRDKVGAYESVGSRPQPNMEVISKLKPDLII 118
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                                                                                                                                                                                                                                                                                                                                                                         246 GPYLOMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKCINAVKNORVDILDR 303
                                                                                                                                                                                                                                                                                                                                                                                                                ADNNRHKGI YKDLNKI APTIELKSFDGDYNENI DAFKTI SKALGKEEEGKKRLEEHDKKI
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APPLICANT Syskind Judith W.
APPLICANT Tranick, John D.
APPLICANT Tranick, John D.
APPLICANT Tranick, John D.
APPLICANT Tranick, John D.
APPLICANT Tranick, John D.
APPLICANT Tranick, John D.
APPLICANT Tranick, John D.
APPLICANT Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR PLLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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295 NKWLKSRGIIASESMAEDLEKIAEK 319
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Patent No. US20020061569Al
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Staphylococcus aureus US-09-815-242-12122
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Best Local Similarity 47.1%
Matches 153; Conservative
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                                                                                                                                                                                                                                                       KDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMD 195
                                                                                                                                                                                                                                                                                           121 KELNKIAPTLSLKSFDGDYKQNINSFKTIAKALNKEKEGEKRLAEHDKLIKKYKDEIKFD 180
                                                                                                                                                                                                                                                                                                                                                                               196 KNOKVLPAVAAKSGILAHPSNSYVGOFLSQLGFKRALSDDVTKGLSKYLKGPYLOMNTET 255
                                                                                                                                                                                                                                                                                                                                                                                                                LSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISS 315
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      LLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVAL
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43.04; Score 726; DB 9; Length 319;
Best Local Similarity 47.14; Pred. No. 2.2e-41;
Matches 153; Conservative 61; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLIING DATE: 2000-03-21
PRIOR PLIING DATE: 2000-05-26
PRIOR PLIING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/223,578
PRIOR PLIING DATE: 2000-10-23
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert

// TYPE: PRT
// ORGANISM: Staphylococcus aureus
US-09-815-242-5249

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US-09-815-242-5249
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Sequence 329, Application US/10470048B

Sequence 329, Application No. US20050037444A1

Publication No. US2005003744AA1

GENERAL INFORMATION:

APPLICANT: MEINKE ET AL.

TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN

FILLE REPERENCE: SONN:03502

CURRENT PILLIOR DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: Patentin version 3.1

SEQ ID NO 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR 310
                                                                                                   244 NEBLANINPKYMILATDGKTDKNRTKF----IDPAVWKSLKAVKDNKVYDVDRNKWLKSR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLIIADNNRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 KIKSELSKIAPTIMLVSGTGDYNANIEAPKTVAKAVGKEKEGEKRLEKHDKILAEIRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 NEELANINPKYMILATDGKTDKNRTKF----IDPAVWKSLKAVKDNKVYDVDRNKWLKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 VVPMLILVVAVAGGGGQKDT----EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
                                                                                                                                                                                                                                                                                                                                                       253 TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR
                                                                         73 VALDVKPYGIADDNKKORIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLIIADNNRHK
                                                                                                                                                                     133 GIYKOLNKIAPTIELKSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGITKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                               193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%; Score 724.5; DB 1
46.9%; Pred. No. 2.8e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 GIIASESMAEDLEKIAEK 317
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300 GIIASESMAEDLEKIAEK 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus aureus US-10-470-048B-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 46.9
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           311
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APPLICANT: Ku, H.
TITLE OF INVESTION: Identification of Essential Genes in Microorganisms iTITLE OF INVESTION: Identification of Essential Genes in Microorganisms iTITLE OF INVESTION: Identification of Essential Genes in Microorganisms of TILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/203
PRIOR PELICATION NUMBER: 60/203,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/267,931
PRIOR PELICATION NUMBER: 60/267,931
PRIOR PELICATION NUMBER: 60/267,636
PRIOR PELICATION NUMBER: 60/267,636
PRIOR PELICATION NUMBER: 60/269,308
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                                                            EBYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOPLSQLGFKEALSDDVTKGLSKYLK 245
                                                                                                                                                              GPYLOMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNORVDILDR 303
                                                                                                                                                                                                                                                   ADNNRHKGI YKDLNKI APTI ELKS PDGDYNENI DAPKTI SKALGKEEEGKKRLEEHDKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 319;
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Best Local Similarity 46.9%; Pred. No. 2.8e-41;
Matches 149; Conservative 63; Mismatches 95
                                                                                                                                                                                                                                                                                                                       DLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                : | : | | : | | | | | | | : : | : : : | NKWLKSRGIIASESMAEDLEKIAEK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44133, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-282-122A-44133
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LENGTH: 319
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13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL 72

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RESULT 10

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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
RIOR APPLICATION NUMBER: 60/191,078
RRICR APPLICATION NUMBER: 60/203,848
RRICR APPLICATION NUMBER: 60/203,727
RRICR APPLICATION NUMBER: 60/203,335
RRICR APPLICATION NUMBER: 60/230,335
RRICR APPLICATION NUMBER: 60/230,347
RRICR APPLICATION NUMBER: 60/230,347
RRICR APPLICATION NUMBER: 60/242,578
RRICR APPLICATION NUMBER: 60/242,578
RRICR APPLICATION NUMBER: 60/253,625
RRICR RILING DATE: 2000-10-23
RRICR RILING DATE: 2000-11-27
RRICR RILING DATE: 2000-11-27
RRICR RILING DATE: 2000-12-22
RRICR APPLICATION NUMBER: 60/257,931
RRICR RILING DATE: 2001-02-09
RRICR RILING DATE: 2001-02-09
RRICR RILING DATE: 2001-02-09
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RRICR RILING DATE: 2001-02-09
RRICR RILING DATE: 2001-02-06
RROMANINGER OF SEQ ID NOS: 78614
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ROMANINGER PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PAREN
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APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Danniel
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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38.1%; Score 644; DB 15; Length 175;
Best Local Similarity 70.9%; Pred. No. 4e-36;
Matches 124; Conservative 23; Mismatches 24; Indels
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| Sequence 66890, Application US/10282122A
| Publication No. US20040029129A1
| GENERAL INFORMATION:
| APPLICANT: Wang, Liangsu
| APPLICANT: Zamudio, Carlos
Sequence 71291, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Staphylococcus haemolyticus US-10-282-122A-71291
                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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APPLICANT: Vanamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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PRIOR PLING DATE: 2001-12-20
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 TISKALGKEBEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOF 222
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.6%; Score 516.5; DB 15; Length 298; Best Local Similarity 38.1%; Pred. No. 3.6e-27; Matches 111; Conservative 65; Mismatches 98; Indels 17;
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; Sequence 56054, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pasteurella multocida
US-10-282-122A-66890
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                             Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
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US20020061569A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 SLGL-----EESIVKRWQQ 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 VGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI 164
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                                                                                                                                                                                                                                                                                                                                                                  PILE OF INVENTIONS: IGENTIFICATION OF ESSENTIAL CHIES IN PLEURENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PLICATION NUMBER: 60/206,846

PRIOR PILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.2%; Score 460; DB 15; Length 3 35.8%; Pred. No. 2.5e-23; ive 60; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 DPVWKKINAVKNQRVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Enterobacter cloacae US-10-282-122A-56054
   Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 35.8%
Matches 101; Conservative
                                                                                                                                                                                                                                                                  Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                   Trawick, John
Carr, Grant
                                                                                                                                                                           Wall, Daniel
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APPLICANT:
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RESULT 13 US-09-815-242-10469 ; Sequence 10469, Application US/09815242

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86 VGTRAQPSLEAIAALKPDLJIADSSRHAGVYIALQQIAPVLLLKSRNETYAENLQSAAII 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.2%; Score 460; DB 9; Length 302
35.5%; Pred. No. 2.5e-23;
tive 62; Mismatches 104; Indels
APPLICANT: Obleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Traminoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Andlone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
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PRIOR FILING DAIE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Escherichia coli
US-09-815-242-10469
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US-10-282-122A-56805
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SEQ ID NO 10469
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272
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Garnt
APPLICANT: Samamoto, Robert
APPLICANT: Samamoto, Robert
APPLICANT: Samamoto, Robert
APPLICANT: Provyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRAN 034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PAPLICATION NUMBER: 60/200,05-26
PRIOR PAPLICATION NUMBER: 60/200,727
PRIOR PAPLICATION NUMBER: 60/200,727
PRIOR PAPLICATION NUMBER: 60/200,335
PRIOR PAPLICATION NUMBER: 60/230,347
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PRIOR PLING DATE: 2000-09-09
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Dublication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Matches 100; Conservative
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US-10-282-122A-69420
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APPLICANT: Travick, John
APPLICANT: Namemoto, Robert
APPLICANT: Namemoto, Robert
APPLICANT: Namemoto, Robert
TILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PELING DATE: 2000-09-06
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PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25, 931
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PRIOR APPLICATION NUMBER: 60/25, 931
PRIOR PELING DATE: 2001-10-21
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US-08-781-986A-5193
; Sequence 5193, Application US/08781986A
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Ohlsen, Kari
Yaskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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TYPE: PRT ORGANISM: Staphylococcus aureus
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US-10-329-624-5193
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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
ATTLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 94.0 Key West Avenue
CITY: Rockville
STATE: Maryland
COUWIRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 IKML-VVTLAFLLV-LAGCSGNSNKQSSDNKDKETTSIKHAMGTTEIKGKPKRVVTLYQG
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; Pred. No. 1.5e-19;
65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: 30,446
TELEPRENCE/DOCKET NUMBER: 90,946
TELEPRONCE (101) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5193: SEQUENCE CHARACTERISTICS: LENGTH: 33 of antho acide TYPE: anino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.0%;
Best Local Similarity 32.8%;
Matches 113; Conservative 6
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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Sequence 16, Application US/10278946 Publication No. US20030153733A1

RESULT 17 US-10-278-946-16

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Sequence 5193, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
GAIL H. Charles Kunsch
GLI H. Choi
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 FQK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAĞEILNDLGFKR-----NKDL 228
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APPLICANT: Simpson et al.
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P8461USD.
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/830,217
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-20
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-05-07
NUMBER: US 60/084,674
PRIOR FILING DATE: 1998-05-07
NUMBER: PACENTION NUMBER: US 60/084,674
PRIOR FILING DATE: 1998-05-07
NUMBER: PACENTION NUMBER: US 60/084,674
PRIOR FILING DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DA
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24.0%; Score 405; DB 14;
Best Local Similarity 32.8%; Pred. No. 1.5e-19;
Matches 113; Conservative 65; Mismatches 132;
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STREET: 9410 Key West Avenue
CITY: Rockville
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SOFTWARE: Patentin version 3.1
                 SEQ ID NO 346
LENGTH: 330
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Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: WEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REPRENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQBPAPNLBEISKLKPDLIVAS 122
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            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: J-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 08/986
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
APPLICATION NUMBER: 46,789
REGISTAATION SUPPRIABILE TELEFAX: (300): 5193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%; Score 405; DB 15; Length 330; 32.8%; Pred. No. 1.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TYPE: proposition acid
TYPE: protein
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 330 amino acida
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Best Local Similarity 32.81
Matches 113; Conservative
  COMPUTER READABLE
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US-10-470-048B-346
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
TITLE REPERENCE: PB461USD2
CURRENT APPLICATION NUMBER: US/10/967,189
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 10/278,946
PRIOR APPLICATION NUMBER: US 09/830,217
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1998-03-18
PRIOR PPLICATION NUMBER: US 60/086,682
PRIOR APPLICATION NUMBER: US 60/080,296
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
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                                                                                Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 VRNNQVSDDLDBITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                          Indels
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                                                                                Query Match 24.0%; Score 405; DB 17;
Best Local Similarity 32.8%; Pred. No. 1.5e-19;
Matches 113; Conservative 65; Mismatches 132;
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; Sequence 16, Application US/10967189
; Publication No. US/0050953995A1
; GENERAL INFORMATION:
; ORGANISM: Staphylococcus aureus
US-10-470-048B-346
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Matches 113; Conservative
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Best Local Similarity
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                                                63 ATDVAVSLGVKPVGAVESWTQKPKPEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                     128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                          188 YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                               241 SKYLKG--PYLOMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLINA 292
                                                                                                                                                                                                                                                                                            68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLBEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAAA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                          289 VKNNQVSDDLDBITWNLAGGYKSSLKLIDDLYB--KLNIEKQSK 330
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR PILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45599, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-45599
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ORGANISM:
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Length 324;

DB 15;

23.1%; Score 391;

Query Match

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72 LVALDVKPVGIADDNKKORIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRH 131
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                                                                                                                                         65 EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKOPNLEEISKLK 120
                                                                                                                                                                   178 LEEHDKKIEEYKKEI----TMDKNOKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                         LADMDKAFADAKAKIEKADLKDKNIAMAQAFTAKNVPTFRILT--DNSLALQVTKKLG-- 230
                                                                                                                                                                                                                                                                                                                                                                                                   230 EALSDDVIKGLSKYLKGPYLOMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                              13 VIGLLFVLIATAACGNNSSSNS-SKESSKDGVEIKHEEGTTKVPKHPKRVVLEYSFVDA
                                                                                    PDLIIADNNRHKGIYKDLNKIAPTIEL---KSFDGDYNENIDAFKTISKALGKEEEGKKR
                                                         9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKD----GVEIKHEEGTTKVPKHPKRVVVL
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                   40;
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                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : : | : : | BELKFKKENKAYKLKGDTWIFG-GPESATSLATQVADV 319
; Pred. No. 1.4e-18; 59; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PLICATION NUMBER: JP 99/377484
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
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US-09-738-626-3875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3875, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90; Conservative
               Matches 116; Conservative
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IKEDA, MASATO
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Best Local Similarity
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11 IAIIGLVTVF---ALGGSKKNESKTSENSNNTIKITHNLGETDVKLNPKKVVVFDYSALD

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                                                                                                                                                                                                                                                                  243 SSENFGOIDGDLIFYTIPGSPEATTYPKISEL-----WVDSPAVRQGRTYEFEDETWWVG 297
                                                               192 ITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQM 251
                                                                                                                                                                                                                                                                                                                                                                                                            252 NTETLSQVNPERMF--IMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARS 309
KGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKKIEEYKKE 191
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PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/267,636
PRIOR PELICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PRIOR PRIOR APPLICATION NUMBER: 92-93
PRIOR PRIOR PRIOR APPLICATION NUMBER: 92-93
PRIOR PRIOR DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.0348
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53267, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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R FILING DATE: 2000-05-23

R PILING DATE: 2000-05-26

R RILING DATE: 2000-05-26

R RILING DATE: 2000-09-06

R PILING DATE: 2000-09-06

R PILING DATE: 2000-09-06

R PILING DATE: 2000-09-06

R PILING DATE: 2000-09-09

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Ohlsen, Kari
Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Daniel
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Best Local Similarity
Matches 99; Conserv
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US-10-282-122A-5326
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APPLICANT: Forestr.
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APPLICANT: AND H.
APPLICANT: AND H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Besential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/200, 848
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-25
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-12-26
PRIOR PRILING DATE: 2001-12-26
PRIOR PLILING DATE: 2001-02-16
PRIOR PLILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                     235 HGQ--NITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKNDNII 292
71 ALVALDVKP--VGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLERISKLKPDLIIADN 128
                                                                                                                    129 NRHKGIYKDLNKIAPTIELKSFDGDYNE----NIDAFKTISKALGKEBEGKKRLEEHDKK 184
                                     PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 ILDRDLW-ARSRGLISSEEM 318
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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; ORGANISM: Bacillus anthracis
US-10-282-122A-46283
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US-10-282-122A-46193
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SEQ 1D NO 45385
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Xu, H.

TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,038

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

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PRIOR PILING DATE: 2000-10-23

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                                                                                                                                                                                                                                                                                                                                                        127 DNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 EYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYV-GQFLSQLGFKEALSDDV----TKGLS 241
                                                                                                                                                  9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                Gaps
                                                            32;
      DB 15; Length 314;
18.5%; Score 313; DB 15; Length 3
29.9%; Pred. No. 2.6e-13;
ive 65; Mismatches 135; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Zamudio, Carlos
APPLICANT: Andlone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Yamamoto, Robert
   Query Match
Best Local Similarity 29.9%
Matches 99; Conservative
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US-10-282-122A-45385
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APPLICANT: AU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2008-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                   232 LSDDV----TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 IPNDLKLPAVKGTP--TDKPLVQVQKEALIDYNPDYLFVFTTGDGSQR--LKEFQEESIW 272
                                                                                                                                                                                                                                                                  118 KLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 LEEHDKKIEEYKKEITMDKNOKVLPAVAAKSG-----LLAHPSNSYVGQFLSQLGFKEA
                                                                                                                                                                                                                                16 LLFVLIAT----AACGNNSSSNS-SKESSKDGVEIKHEEGTTKVPKHPKRVVVLBYSFVD
                                                                                                          Length 314;
                                                                                                                                                                     66; Mismatches 106; Indels
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
TYPE: PRT ORGANISM: Bacillus anthracis
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Yamamoto, Robert
Forsyth, R.
                                                                                                                Query Match
Best Local Similarity 27.3*
Matches 93; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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APPLICANT: XU, H.

TITLE OF INVENTION Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR PLICATION NUMBER: 60/207,727
PRIOR PRILING DATE: 2000-05-23
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-09-06
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/230,336
PRIOR PLILNG DATE: 2000-11-27
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-20
PRIOR PLILNG DATE: 2000-10-20
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PRIOR PLING DATE: 2001-02-09
DKKKISNTVEVPKNPKNAVVLDÝGALDVL----KELGVADKVKGLPKGENNQSLPKFLD 115
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                                                                                                                 155 NENI--DAFK---TISKALGKEEEGKKRLEEHDKKIBEYKKEITMDKNOKVLPAVAAKSG 209
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                                                                               --KIGKYTSVGTRKQPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDY 154
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-68785
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339 IDELNE 344
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SEQ ID NO 68785
LENGTH: 342
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APPLICANT: DOUGETE-Stamm, Lynn
APPLICANT: DOUGETE-Stamm, Lynn
APPLICANT: DOUGETE-Stamm, Lynn
APPLICANT: DOUGETE-Stamm, Lynn
APPLICANT: Bush, David
TITLE OF INVENTION: EPIDERHIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-16
CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-134,001
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PDLIIADNNRHKGIYKDLNKIAPTIEL---KSFDGDYNENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEEHDKKIEBYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 LADMDKAFADAKAKIEKADLKDKNIAMAQAFTAKNVPTFRILT--DNSLALQVTKKLG-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 BWVYSEDLIALGVQPVGMADIKNYNKWVNTKTKPSKUVV----DVGTRQQPNLEBISRLK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EGTTKVPKHPKRVVVLEYSPVDALVALDVKPVGIADDNK-----KNRIIKPLRD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Gape
     PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTHARE: Patentin version 3.1
SEQ ID NO 46193
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKES-SKDGVEIKHE---
                                                                                                                                                                                                                                                                                                                                          Length 264;
                                                                                                                                                                                                                                                                                                                                    ; Score 300; DB 15; Length 20; Pred. No. 1.6e-12; 50; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7181, Application US/10724972A Publication No. US20040147734A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Match 17.8%;
Local Similarity 33.6%;
hes 93; Conservative 5
                                                                                                                                                                                                                                                 , ORGANISM: Bacillus anthracis
US-10-282-122A-46193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: S.epidermidis
US-10-724-972A-7181
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US-10-724-972A-7181
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LENGTH: 351
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Best Local S
Matches 93
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GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                       238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                              126 ADNNRHKGIYKDINKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                          68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLII
                                                                                                                                                                                                                                                                                         122 I-SGROODYOEQLKAIAPTIYLAVDAKNPWASTKONIETLGTI---FDKEEVAKEKITGL
                                                                                                                                                                                                                                                                                                                                                                         178 EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST
                                                                                                                                                                                                           67 SLDTMDALGVGDRVVGAPTKN----IPAYLKKYQKVESAGGIKEPDLEKINQLKPDLII
                                                                                                                                                                                                                                                                                                                                    182 DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT
                                                                                  11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
  Length 317;
                                             IndelB
Query Match
16.7%; Score 283; DB 9; L
Best Local Similarity 30.4%; Pred. No. 2.9e-11;
Matches 101; Conservative 59; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 KVIMLQPDVWYLSGGGLESMHL---MIEDVKK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1996-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 38, Application US/10206576 ; Publication No. US20030017495A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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US-10-206-576-38
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Publication No. US20020045737A1
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 GSHGNI-----VNSELLLKINPDWMFVIDRDAAIGREDSQPA-KQVLDNALVRKVNAWN 306
                                                                                                                                                                                                                      EEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTK 238
                                                                                                                                                                                                                                                                                                                                                                                        LIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAF----KTISKALGKEEGKKRL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                GLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVWKKLNAVK 294
                                                                                                                                            27 KSLSPLFLLLSSLVIAGCDNAQDTSTIQSTEKQTLTIEHAQGTTBIPAHPQKVVVMNMET 86
                                                                                                              9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF 68
                                                                                                                                                                                                69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYT----SVGTRKOPNLEEISKLKPD
                                                                       34;
                              Length 342;
                              17.5%; Score 296; DB 15; Length 3
29.2%; Pred. No. 4.2e-12;
ive 66; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: A. AnderE Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET WINBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 317 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                         90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-071-035-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
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                              Query Match
Best Local Similarity
Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                  11 VSMMGLIMI----SACQTNKKTADSATTETTAKTEVTVKDTNGQLTVPKNPKKVVVFDNG
                                                                                                                                                                                                                                                                                                                                                                                                                        178 EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST
                                                                                                                                                                                                                                                                                 11 LSVIGILIFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                        68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLII
                                                                                                                                                                                                                                    Indels 42; Gaps
                                                                                                                                                                              Query Match
16.7%; Score 283; DB 17; Length 317;
Best Local Similarity 30.4%; Pred. No. 2.9e-11;
Matches 101; Conservative 59; Mismatches 130; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Korst.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tamoro, Robert T.
APPLICANT: Xu, H. Howard
FILLE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILLING DATE: 2000-10-23
PRIOR PILLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PILLING DATE: 2000-12-22
PRIOR PILLING DATE: 2000-12-22
PRIOR PILLING DATE: 2000-12-22
PRIOR PILLING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SOUTHARE: RESERRED FOR WINDOWS VERSION 4.0
SEQ ID NO 10905
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 KVIMLQPDVWYLSGGGLESMHL---MIEDVKK 314
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10905, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
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Publication No. US20050043528A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 14200 Shady Grove Road
                                                                                                                                                                                                                                                                                       68 FVDALVALDV - KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKFDLII 125
                                                                                                                                                                                                                                                                                                                                                                                                                             DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 HGQS------VSYEYVLEKNPGILFVVDRTKAIGGDDSKDNVAANELIQKTDAGKND 285
                                                                                                                                                                                                                                                                                                                                          67 SLĎTMDÁLGÝGDRVÝGAPTKN----IPAYLKKYQKVESAGGIKEPDLEKINQLKPĎLII 121
                                                                                                                                                                                                                                                                                                                                                                                             126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                      11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                    42;
                                                                             16.7%; Score 283; DB 14; Length 317; 30.4%; Pred. No. 2.9e-11; ive 59; Mismatches 130; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATLON APPLICATION NUMBER: US 10/206,576
FILING DATE: 2002-07-29
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-06-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 KVIMLQPDVWYLSGGGLESMHL---MIEDVKK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369PID2
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/912,362
FILING DATE: 06-Aug-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 2000
SOFTWARE: ASCII Text
  SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 317 amino acids
                                                                           Query Match
Best Local Similarity 30.4%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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US-10-206-576-38
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US-10-912-362-38
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STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20850
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STREET: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-09-071-035-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227
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                                                                                                                                                                                                                           68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLII 125
                                                                                                                                                                                                                                                                                                                                                                                        DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSOLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                        178 EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKTLNAVKNQ 296
                                                                                                                                                                                                                                            126 ADNNRHKGIYKDINKIAPTIEL----KSFDGDYNENIDAPKTISKALGKEEEGKKRLEEH 181
                                                                                                                                        11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                   11.VSMMGLIAL---SACQTNKKTADSATTETTAKTEVTVKDTNGQLTVPKNPQKVVPDNG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                      Gaps
                                                                                                   42;
                                                               Length 317;
                                                         Query Match
16.5%; Score 279; DB 9; Length 31
Best Local Similarity 30.1%; Pred. No. 5.4e-11;
Matches 100; Conservative 60; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46179, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION UNMER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION UNMER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION UNMER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION UNMER: 60/267,636
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
; ORGANISM: Enterococcus faecalis US-09-815-242-10905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-46179
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APPLICANT:
APPLICANT:
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Sequence 40, Application US/09071035
Publication No. US20020045737A1
GENERAL INFORMATION:
APPLICANT:
TILE OF INVENTION:
FUNDER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       71 ALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 DKKIEBYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 KYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLK----ELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 HKGIYKDLNKIAPTIE-----LKSFDG--DYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                  10 AILSIFFLLIGCSAKGDEKASATKTEKGKEKIEVTDLSGRKVTFDKVFESFATLSMGDMN
                                                                                                                                                                                                                                                                                                                      12 SVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEG-TTKVPKHPKRVVVLEYSFVD
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 46179 LENGTH: 315
                                                                                                                                                                                                                     Query Match
16.2%; Score 274.5; DB 15; Length 315;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 92; Conservative 70; Mismatches 129; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 RVDILDRDLWARSRGLISSEEMAKELVELSKKDSKK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SBE: Human Genome Sciences, Inc.: 9410 Key West Avenue Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PB369P2
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 ORGANISM: Bacillus anthracis
US-10-282-122A-46179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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US-10-912-362-40

| Sequence 40, Application US/10912362
| Sequence 40, Application US/10912362
| Publication No. US20050043528A1
| Publication No. US20050043528A1
| TITLE INFORMATION: Enterococcus faecalis Polynucleotides and Polypeptides
| TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
| TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
| TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
| TITLE OF INVENTION: ADDRESS: 497 |
| CORRESPONDENCE ADDRESS: ADDRESS: Human Genome Sciences, Inc. CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 GIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GAPTKN-----IPAYLKKYQKVESAGGIKEPDLEKINQLKPDLII-SGRQQDYQEQLKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 IAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 TETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 NOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VTKGLSKYLKGPYLQMN 252
                                                                                                                                                                                                                                                                                                                                                                                                                26 CGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV--KPV
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                               Length 296;
                                                                                                                                                                                                                                                                               Query Match 15.9%; Score 268; DB 14; Length 2
Best Local Similarity 30.3%; Pred. No. 2.8e-10;
Matches 96; Conservative 54; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 10/206,576
FILING DATE: 2002-07-29
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 2.96 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/912,362
PILING DATE: 06-Aug-2004
PRIOR APPLICATION DATA:
                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-206-576-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 2000
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 LISSEBMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 GLESMHL---MIEDVKK 293
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COMPUTER READABLE FORM:
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Sequence 4.0. Application US/10206576
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
VUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryand
                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                GIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GAPTKN-----IPAYLKKYQKVESAGGIKEPDLEKINQLKPDLIII-SGRQQDYQEQLKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 IAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 NOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VTKGLSKYLKGPYLQMN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 TETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRG 311
                                                                                                                                                                                                                                                                                                                                         26 CGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV--KPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEASTHGQS-----VS
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                          Length 296;
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1 Similarity 30.3%; Pred. No. 2.8e-10;
96; Conservative 54; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTHARE: ASCII Text
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-U1-2002
CLASSIFICATION NUMBER: US/09/071,035
PRIOR APPLICATION NUMBER: US 09/071,035
PILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
PILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-05-10
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REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 LISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GLESMHL---MIEDVKK 293
     SEQUENCE CHARACTERISTICS:

JENGTH: 296 amino acide
TYPE: amino acid
STRANDEDNESS: single
JOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-206-576-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172
                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                               Matches
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ORGANISM: Corynebacterium glutamicum
                                                 ; ORGANISM: COLYI
US-09-738-626-4403
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 IAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||| | |: :||: || |: :||: ||: ||: :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 N-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEASTHGQS-----VS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 GIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLANK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.3%; Pred. No. 2.8e-10;
Matches 96; Conservative 54; Mismatches 129; Indels 3
        FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REPRENCE/DOCKET NUMBER: PB369P1D2
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERIŞTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NATAGEMA, SATOSHI
APPLICANT: NATAGEMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HYYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TYKOI, HANUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TREDA, MASATO
APPLICANT: OZAKI, AKI
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-912-362-40
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      LENGTH: 296 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 LISSEEMAKELVELSKK 328
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LENGTH: 306
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73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TETLSQVNPERMFI-----MTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDL 305
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APPLICANT: POMDEJUS. MARK
APPLICANT: POMDEJUS. MARK
APPLICANT: Schoder. Bartwig
APPLICANT: Schoder. Hartwig
APPLICANT: Schoder. Bartwig
APPLICANT: Schoder. Bartwig
APPLICANT: Schoder. Bartwig
APPLICANT: Schoder. Oskar
APPLICANT: BADEFRAUER. GREGOR
TITLE OF INVENTION: CONVERBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
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TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: UNMERR: 05/06.2,787
PRIOR PLICATION NUMBER: DE 19931454.3
PRIOR PLICATION NUMBER: DE 19931454.3
PRIOR PLICATION NUMBER: DE 19931563.9
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-09
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PRIOR PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-09
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SEQ ID NO 572
LENGTH: 306
                                                                               40;
       DB 9; Length 306;
Query Match
Best Local Similarity 25.9%; Pred. No. 4e-10;
Matches 82; Conservative 60; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 DVEGKTVNMIRPRDEQTMSLYGPTSFAGSSLECAG----
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; Sequence 572, Application US/10627476
; Publication No. US20040030116A1
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; UKGANISM: BULALIO
US-10-282-122A-47311
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Best Local S
Matches 93
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-21
PRIOR PLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-36
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-010-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-29
PRIOR PLING DATE: 2000-110-29
PRIOR PLING DATE: 2000-110-20
PRIOR PLING DATE: 2000-110-20
PRIOR PLING DATE: 2000-110-20
PRIOR PLING DATE: 2000-110-20
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PRING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                    VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK 132
                                                                                                                                                                                                                                                                            TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 TETLSQVNPERMFI------MTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDL 305
                                                                                                                                                                                                                                                                                                                                       GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVEGKTVNMIRPRDEQTMSLYGPTSFAGSSLECAG-------LITPDQEWK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 DDLQADIAPENFMLATADYVEVTATDVTDENELPEVIRE-----NREQFPSLTLVDTSY 281
                                                                                                                                                                                          11 LIVLLAAALPLTACSSSSEERASTSSATR--EPTDAHGTTEVPENPQRVVVLEPLELDTA 68
                                                                                                                                                                  17 LFVLIATA----ACGNNSSSNSSKESSKDGVEIKHEEGTIKVPKHPKRVVVLEYSFVDAL
                                                                                                                           Gaps
                                                                                                                           40;
                                                                                  DB 15; Length 306;
                                                                                15.7%; Score 266; DB 15; Length 3 llarity 25.9%; Pred. No. 4e-10; Conservative 60; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 47311, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
p TYPE: PRT
p ORGANISM: Corynebacterium glutamicum
US-10-627-476-572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WARSRGLISSEEMAKEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WVSGVGPLGGSKVLEDI 298
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
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Forsyth, R.
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                                                                                Query Match
Best Local Similarity
Matches 82; Conserv
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US-10-282-122A-47311
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APPLICANT: Wyerh
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYP
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AMI 00649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFFWARE: Patentin version 3.1
SEQ ID NO 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 47311
LENGTH: 342
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Publication No. US20040110181A1
GENERAL INFORMATION:
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ORGANISM: Burkholderia cepacia
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28.9%;
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Matches 86, Conserv
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Search completed: August 25, 2005, 09:40:02 Job time : 166 secs
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284 ALQKDPLLGKINAIKNGAVAVI 305
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2005, 09:18:46; Search time 167 Seconds (without alignments) 775.837 Million cell updates/sec Run on:

Perfect score:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK 335 Sequence:

BLOSUM62 . Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched: 2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database :

geneseqp20008:*
geneseqp20018:*
geneseqp20028:*
geneseqp20038:*
geneseqp200388:*
geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMADIES

					SUMMARIES	
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	1690	100.0	335	. &	ADS07057	Ads07057 Staphyloc
10	1668	98.7	331	v	ABU43214	
וח	1242	73.5	337	4	AAU36661	Aau36661 Staphyloc
4	1233	73.0	337	9	ABR41865	Abr41865 Staphyloc
ហ	1232	72.9	327	9	ABU15904	
v	1228	72.7	337	9	ABR38894	Abr38894 Surface e
7	1214	71.8	348	9	ABM73426	
60	1181	69.9	309	4	AAU33963	Aau33963 Staphyloc
6	726	43.0	319	4	AAU33753	
10	726	43.0	319	4	AAU36529	Aau36529 Staphyloc
11	724.5	42.9	319	9	ABJ19052	Abj19052 Pathogen
12	724.5	42.9	319	ø	ABU16209	
13	724.5	42.9	325	9	ABR38895	
14	724.5	42.9		9	ABR41867	
15	724.5	42.9	325	9	ABM72855	
16	644	38.1		ø	ABU43367	Abu43367 Protein e
17	516.5	30.6		9	ABU38966	_
18	476	28.2	303	9	ABM68354	Abm68354 Photorhab
19	460	27.2		9	ABU28130	Abu28130 Protein e
20	460	27.2	302	4	AAU34876	Aau34876 E. coli c
21	460	27.2		9	ABU28881	
22	454	26.9		9	ABU41496	Abu41496 Protein e
23	405	24.0		7	AAW89745	
24	405	24.0	e	~	AAY42331	Aay42331 Staphyloc
25	405	24.0	330	8	AAY31824	Aay31824 Staphyloc

		Abr41864 Staphyloc	'n	Abul7675 Protein e	Abg08851 Novel hum	Abg13148 Novel hum		Aag90121 C glutami					Abu18269 Protein e	Abp40647 Staphyloc	Ads07886 Staphyloc	Abu40861 Protein e	Adf06577 Bacterial	S.	Aag81684 S. epider
6 ABJ19069	6 ABR38893	6 ABR41864	7 ADF43556	6 ABU17675	4 ABG08851	4 ABG13148	6 ABM73050	4 AAG90121	6 ABU25343	6 ABU18359	7 ADC94889	6 ABU17461	6 ABU18269	5 ABP40647	8 ADS07886	6 ABU40861	7 ADF06577	4 AAG82087	4 AAG81684
330	330	330	330	324	1132	932	287	315	321	314	352	314	264	351	351	342	351	347	347
24.0	24.0	24.0	24.0	23.1	22.2	20.7	20.3	19.6	19.3	18.5	18.2	17.8	17.8	17.5	17.5	17.5	17.5	17.3	17.3
405	405	405	405	391	375	350	343	331	327	313	307.5	301	300	296.5	296.5	296	296	292	292
56	27	28	29	30	31	32	33	3.4	35	36	37	38	39	40	41	42	43	4	45

ALIGNMENTS

antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; Staphylococcus epidermis polypeptide seqid 6352. ADS07057 standard; protein; 335 AA (first entry) computer based system. 04-NOV-2004 ADS07057; RESULT 1 ADS07057

Staphylococcus epidermidis.

US2004147734-A1.

29-JUL-2004.

97US-0064964P. 98US-00134001. 99US-00450969. 01-DEC-2003; 2003US-00724972 08-NOV-1997; 13-AUG-1998; 29-NOV-1999;

(DOUC/) DOUCETTE-STAMM L. (BUSH/) BUSH D.

Bush D; Doucette-Stamm L,

WPI; 2004-580138/56. N-PSDB; ADS03285.

New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.

Claim 17; SEQ ID NO 6352; 741pp; English

The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector, a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a

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aubject for S. epidermidis infection; a recombinant or arriver. Treating a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypoptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus nucleic acid in a sample; a computer readable medium having recorded in it the nucleotide equences with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome of the Staphylococcus genome of the Staphylococcus genome of commercial important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcal epidermidis bacterial confidencial in the amino acid sequence of a S. epidermids protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8; Length 335;
      vaccine composition for prevention or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1690; DB 8;
100.0%; Pred. No. 1.5e-129;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention.
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$$$$$$$$$$$$$$$$$$$$$$$$
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screening

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

'n'n

Wang Wall

N-PSDB; ACA47084

08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, 2003-029926/02.

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                                               GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKR
                                                                   GVESVRGLKILSVIGLLFVVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKR
                                                                                                               WVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLK
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               Gaps
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             Indels
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Best Local Similarity 100.
Matches 335; Conservative
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Antisense, prokaryotic essential gene, cell proliferation; drug design. Protein encoded by Prokaryotic essential gene #28741. ABU43214 standard; protein; 331 AA 21-MAR-2002; 2002WO-US009107 Staphylococcus epidermidis. (first entry) WO200277183-A2 19-JUN-2003 03-OCT-2002 ABU43214; ABU43214 SERVICE SERVIC

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cancileded are:

(2) a vector comprising a promoter operably linked to the nucleic acid cancileded are:

(3) an isolated acid and promoter operably linked by the antisense cancileded are:

(4) an abost cell containing the vector; (3) an isolated polypeptide; (5) publicing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pethway or required for proliferation, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pethway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for the strains is present in a culture or collection of the strains is present in a culture or collection of strained for proliferation in cells other changed cards required for proliferation in cells other than S. aureus, S. typhimurium, contained for proliferation in cells other than S. aureus, S. typhimurium, contained that directify from NIPO at equence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this part directify from NIPO at equence is encoded by one of the contained of the contained of the proliferation of the printed sequence is encoded by one of the contained of the contained of
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Pred. No. 9.2e-128;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                      25; SEQ ID NO 71138; 1766pp; English.
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Best Local Similarity 99.7%;
Matches 330; Conservative 1
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4 SVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV
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241 KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr GJ;
                                                                                                                                                                                                                                                                         Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                              Staphylococcus aureus cellular proliferation protein #831.
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                              LWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                     LWARSRGLISSEEMAKELVELSKKOSKKONK 331
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                                                                                                                                               AAU36661 standard; protein; 337
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2000US-020648P.
2000US-0207727P.
2000US-0253625P.
2000US-0253625P.
2000US-0257911P.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
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N-PSDB; AAS54520.
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
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Best Local Similarity 72.04 Matches 236; Conservative

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The present sequence is that of a novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP). To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisers. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The present SEIP has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods be used indantification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop
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10 TWRGLKTFSILGLIVALFLVAACGNTDNSSKKESSTKDTISVKDENGTVKVFKDAKRIVV
                                                                  10 LEYSFADALAALDVKPVGIADDGKKKRIIKPVREKIGNYTSVGTRKQPNLEEISKLKPDL
                                                                                                                   124 IIADNNRHKGIYKDLNKIAPTIELKSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDK
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                                                  LEYSFVDALVALDVKPVGI ADDNKKNRI I KPLRDKIGKYTSVGTRKOPNLEBISKLKPDL
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                                                                                                           70 LEYSFADALAALDVKPVGIADDGKKKRIIKPVREKIGDYTSVGTRKQPNLEEISKLKPDL 129
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                                                                           4 SVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV
                                                                                                  LEYSFVDALVALDVKPVGIADDNKKNR11KPLRDKIGKYTSVGTRKQPNLEEISKLKPDL
                                                                                                                                   1 I ADNNRHKGI YKDLNKI APTI ELKSFDGDYNEN I DAPKTI SKALGKEEEGKKRLEEHDK
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                                                 Gaps
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                                Length 337;
                                                 50; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #1431.
                               73.0%; Score 1233; DB 6;
larity 71.6%; Pred. No. 3.3e-92;
Conservative 43; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
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                                                                                                                                                                                                                                               DLWARSRGLISSEEMAKELVELSKKDSK 331
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; ACA19774.
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Trawick JD,
                                         Similarity
diagnostic assays
                 Sequence 337 AA;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway in which a proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene product or that has an activity against a biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene product is compound; a activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for proliferation in cells other candidate molecules for rational correlated for proliferation in cells other candidate molecules acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumonlae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent directly from NIPO at cellular directly fired missions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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Matches 235; Conservative
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Staphylococcus aureus protein #2666.
20-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolating microbial target surface exposed immunogenic polypeptides, by immunizing host with microbial membrane-associated polypeptides to produce antibodies and using antibodies to isolate target polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of target surface exposed immunogenic polypeptides (SEIP) from microorganisms. The SEIP's of the invention are receptors of iron-binding molecules. The activity of polypeptides of the invention may be described as antibacterial, fungicide and protozoacide. Pharmaceutical compositions based on the polypeptides of the invention are useful for treating infections and diseases caused by microbes including bacteria, fungi and protozoa in a patient. They are also useful for topical disinfection in an animal or mammal e.g. human. The current sequence represents an SEIP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 TWRGLKTFSILGLIVALLLVAACGNTDNSSKKESSTKDTISVKDENGTVKYPKDAKRIVV
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SEIP; surface exposed immunogenic polypeptide; iron-binding; receptor; antibacterial; fungicide; protozoacide; infection; disinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SVRGLKILSVIGLLFVLLATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 40-41; 46pp; English
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Best Local Similarity 71.3
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scott DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, useful as a vaccine for treating or infection, specifically an infection caused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 KPFSILGLIVALLLVAACGNTDNSSKKESSTKDTISVKDENGTVKVPKDAKRIVVLEYSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKEI TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPY
Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Scarselli M;
                                                                                                                                                                                                                                                               27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                     27-MAR-2001; 2001GB-0007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing Staphylococcal
S. aureus, e.g. sepsis.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety
            KDLNKI APTI ELKSFDGDYNENI DAFKTI SKALGKEEEGKKRLEBHDKKI EEYKKEI TMD
                                                                                                                  241 LADLNPERMIIMTDNAKKDSAEFKKLQEDPTWKKLNAVKNNRVDIVDRDVWARSRGLISS
                                    256 LSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISS
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Xu HH;
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2000US-0207727P.
2000US-0242578P.
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Yamamoto RT,
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                 AAU33963 standard; protein; 309 AA
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2000US-0207727P.
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16-FEB-2001; 2001US-0269308P.
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Xu HH;
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N-PSDB; AAS51822.
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Best Local Similarity
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26-MAY-2000;
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Yamamoto RT,
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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Best Local Similarity 47.1%; Pred. No. 8e-51;
Matches 153; Conservative 61; Mismatches 99; Indels
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N-PSDB; AAS54388.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes chair use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coil, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Seudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins, and to obtain antisense nucleic acid sequence is also useful to screen for homologous curisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful corrections of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent of the printed specification, but was obtained in celectronic format directly from WINDO at cellular proliferation protein. Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathogen specific antigen related staphylococcal protein SEQ ID No 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 ADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPYLQMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%; Score 726; DB 4; Length 31
47.1%; Pred. No. 8e-51;
Ltive 61; Mismatches 99; Indels
Example 3; SEQ ID NO 12122; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 DLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | :|||:|| || || || 293 NKWLKSRGIIASESMAEDLEKIAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.1%
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-2003
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ABJ19052
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ABU16209 standard; protein; 319 AA

ABU16209

ABU16209;

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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the casequences of 53-2261 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a paramecutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament contracting to preventing staphylococcal infections or colonisation against S. epidermidis. The antibody preparations may also be used for disgnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 NEELANINPKVMILATDGKTDKORTKF----IDPAVWKSLKAVKDNKVYDVDRNKMLKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
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                                                                                                                                                                                                                                                                                                                                                     Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 319;
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                                                                                                                                                                                                                                                                                                                                                 Klade C, Henics T,
ryla A, Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.16-50;
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46.9%; Pred. No. 1.1e-
ive 63; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Von Ahsen U, Klade C
O, Etz H, Dryla A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 212; 252pp; English.
                                                                                                                                                                                                                                                                               (CIST-) CISTEM BIOTECHNOLOGIES GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|:|| ||::|
GIIASESMAEDLEKIAEK 317
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                                                                                                                                                                                                         26-JAN-2001; 2001AT-00000130.
                                                                                                                                       21-JAN-2002; 2002WO-EP000546.
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Matches 149, Conservative
                                                                                                                                                                                                                                                                                                                                                 Meinke A, Nagy E, Von
Minh DB, Vytvytska O,
Tempelmaier B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-075410/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 319 AA;
WO200259148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preparation.
                                                              01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133
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The 613 antisense aequences given in the specification where expression of the 613 antisense aequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibitited by the proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway confirmed for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies they are required for relular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or granism acts; (9) manufacturing an antibiotic; (10) profiling a corganism acts; (13) acuturing an antibiotic; (10) profiling a corganism acts; (13) identifying the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the except of a compound that inhibits the compound acts; (13) identifying the farget of a compound that inhibits of collection of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, X. premoniae or P. acruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Willey are sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                    Protein encoded by Prokaryotic essential gene #1736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 44133; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                              06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0362699P
                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                            19-JUN-2003 (first entry)
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                                                                                                                                                                        Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02.
N-PSDB; ACA20079.
                                                                                                                                                                                                                  WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                              21-MAR-2001;
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Staphylococcus aureus.
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N-PSDB; ACC48534.
                                        Sequence 325 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2003.
                   invention
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                                                            Query Match
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                                                                                                                  63
                                                              72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolating microbial target surface exposed immunogenic polypeptides, by immunizing host with microbial membrane-associated polypeptides to produce antibodies and using antibodies to isolate target polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of target surface exposed immunogenic polypeptides (SEIP) from microorganisms. The SEIP's of the invention are receptors of iron-binding molecules. The activity of polypeptides of the invention may be described as antibacterial, fungicide and protozoacide. Parmaceutical compositions based on the polypeptides of the invention are useful for treating infections and diseases caused by microbes including bacteria, fungi and protozoa in a
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEIP; surface exposed immunogenic polypeptide; iron-binding; receptor; antibacterial; fungicide; protozoacide; infection; disinfection.
                                                                                                                                                                                                                                           73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK
                                                                                                                                                         193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
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                                                                                                                                                                                                                                TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR
                                                              13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                133 GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI
                                          Gaps
                                         11;
                    Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                             exposed immunogenic polypeptide (SEIP) # SEQ ID 21.
                                          IndelB
                     DB 6;
                     42.9%; Score 724.5; DB 6
46.9%; Pred. No. 1.1e-50;
                                         63; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  ABR38895 standard; protein; 325
                                                                                                                                                                                                                                                                          GLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                      300 GIIASESMAEDLEKIAEK 317
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                          Conservative
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                             Local Similarity
es 149; Conserv
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   Sequence 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP). To isolate SEIP genes, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQSTLKSAFAPGISRAGMFINNEDTFWGQFLIKWGIQPEVTKDKTTHVGERKGGPYIXLN
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patient. They are also useful for topical disinfection in an animal mammal e.g. human. The current sequence represents an SEIP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                          Length 325
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                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 724.5; DB 6
46.9%; Pred. No. 1.1e-50;
ive 63; Mismatches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 46.94
Matches 149; Conservative
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antieera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The present SEIP has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
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screened with anti-SEIP
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                     11;
                                                                                                                                                                                         Length 325;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                        95;
expression library of S. aureus genomic DNA was
                                                                                                                                                                                         42.9%; Score 724.5; DB 6
46.9%; Pred. No. 1.1e-50;
                                                                                                                                                                                                                      63; Mismatches
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GIIASESMAEDLEKIAEK 323
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                                                                                                                                                                                                                        Conservative
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N-PSDB; ACF74415.
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                                                                                                                                                                                                         Similarity
                                                                                                                                 diagnostic assays
                                                                                                                                                                Sequence 325 AA;
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310
                                                                                                                    ocaphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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preventing Staphylococcal infection, specifically an infection caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 724.5; DB 6;
llarity 46.9%; Pred. No. 1.1e-50;
Conservative 63; Mismatches 95;
                                                                                   Claim 1; SEQ ID NO 4190; 49pp; English.
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06-SEP-2001; 2001US-00948933.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
06-MAR-2002; 2002US-0362699P.
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                                S. aureus, e.g. sepsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 325
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ABU43367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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Protein encoded by Prokaryotic essential gene #24493

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the invention fractates to an isolated in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular cropificration or the activity of a gene in an operon required for proliferation or that that an equival influence the activity of compound that influence the activity of identifying a gene required for cellular proliferation, (8) required for proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or undersexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the strains is present in a culture or collection of compound section of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the confidentifying proteins or screening for homologous nucleic acids are useful for required for proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained for this properation of the printed specification, but was obtained for this contained for the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                 Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any
                                                                                                 Ohlsen KL,
Forsyth RA,
                                                                                                 Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 71291; 1766pp; English.
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                                                                                            Malone C,
Carr GJ,
(ELIT-) ELITRA PHARM INC
                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                           2003-029926/02
                                                                                                                                                                                                                                                                                         N-PSDB; ACA47237.
                                                                                            Wang L,
Wall D,
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5 VRGLKILSVIGLLFVLIATAACGNNSSSNS----SKESSKDGVEIKHEEGTTKVPKHPKR 60 1 HKGFKFAGIVALLFALVLVTACGNVSNNGSGDSGNKSSSKDSIKIKHELGTTKVPKDAKR 60 Gaps 4 38.1%; Score 644; DB 6; Length 175; 70.9%; Pred. No. 1.8e-44; ive 23; Mismatches 24; Indels Best Local Similarity 70.98 Matches 124; Conservative Sequence 175 AA; Query Match 8 셤

61 VVVLEYSFVDALVALDVKPVGIADDNKKORIIKPLRDKIGKYTSVGTRKQPNLEBISKLK 120

ABU38966 standard; protein; 298 AA. (first entry) 19-JUN-2003 ABU38966; ABU38966

RESULT 17

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the nucleic acid inhibits proliferation of a cell. Also included are:

the folla antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

the folla antisense sequences given in the specification where expression is contained by the antisense prolypeptide whose expression is inhibited by the antisense cartisense containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense cartisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the cartistic or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) aculture compound that inhibits proliferation of an organism; or the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the creative compound; or an organism. The antisense nucleic acids are useful for dear definite proliferation of an organism. The antisense moleic acids are useful for for cillular proliferation of solver is observable or isolate candidate molecic acids required for cillular proliferation of solver is a candidate molecic acids required for cillular proliferation of solver is the sequence of a compound or acids required to a sequence of a compound or a collection of an organism. The antisense mucleic acids are useful for four definitions of the strains of solvers and decomposition or an action of an organism. The antisense are acids required to a sequence of a compound organism or servening for homologous nuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 VEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium
                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.6%; Score 516.5; DB 6; 38.1%; Pred. No. 9.5e-34; live 65; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 66890; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                     06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242
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Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02
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proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the CO splypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that the container, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Co luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as inserticides, bactericides and fungicides. The companies of proteins, vectors contraining the genes and Ab are also useful charapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as
                                                                                                                                                                                                                                                                                 LSQLGFK--EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKE 280
                                           143 KIGDLIGKSKEMQARIAKHKQDIADIAK--TLPKGKKAIIGVSRETQFNLYNSESYAGGL 200
                                                                                                                                                                                                                                                                                                                             201 VEVLGYQMPKARADN------QPNASVGLBQVAABKPDLMILIHYR---DESIARK 247
TSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial, fungicide, insecticide, polymorphism, genetic analysis, detection, food, gene expression, plant, animal, microorganism, toxin, antibiotic, biopesticide, virulence factor, disease model, plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                          TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus luminescens protein sequence #1451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaser P, Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2, SEQ ID NO 1451; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM68354 standard; protein; 303 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP.) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001; 2001FR-00001659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Photorhabdus luminescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       whooping cough.
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                                                                                                                                                                                                                             LSOLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSOVNPERMFIMTNKASSNEPSLKELE 282
                                                                                                                                                                                                                                                                                                                                           202 LTALGLKVPASVN------HAAMVSLNLEQLIALNPDWLIVAHYR---QESIVKRWQ 249
biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                      43 VEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKY
                                                                                                                                                                    24 VIVQDEGGSFILMTVPQRVVVLELSFADALAAINISPVGIADDNDPQRILIDVRQRIKPW
                                                                                                                                                                                                                                                                                     163 TISKALGKEBEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid comprising any one
                                                                                                                             Gaps
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                Ouery Match 28.2%; Score 476; DB 6; Length 303; Best Local Similarity 36.0%; Pred. No. 2e-30; Matches 102; Conservative 60; Mismatches 107; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                 283 KDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
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Forsyth |
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Yamamoto R,
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Trawick JD, Carr GJ,
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25-OCT-2001; 2001US-0342923P.
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06-MAR-2002; 2002US-0362699P
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                                                                       Sequence 303 AA;
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway capathed for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies car a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which the extent to which each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of the strains is present modeled acids required for cellular proliferation of the strains of the compound of a compound of an organism. The antisense nucleic acids required for cellular proliferation of an organism candidate modeled and acid actional actions of the strains of the compound organism and the cellular proliferation of the strains of the compound organism and the cellular proliferation of the strains of the cellular proliferation of the strains of the cellular proliferation of the cellular proliferation o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. arruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 SLGL------NVPAAMAGASMPSIGLEQLLAVNPAWLLVAHYR---EESIVKRWQQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 DPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVEL 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.2%; Score 460; DB 6
35.8%; Pred. No. 4e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can entibodies capable of binding to the expressed proteins. The proteins can entibodies also useful to screen for homologous oncleic acids which are required for cell proliferation in a wide variety of of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent call directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEMVGKKREMOARLEOHKERMAOWASO--LPKGTRVAFGTSREQOFNLHTGETWTGSVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 VQDEHGTFTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS
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                                                                                                                                                                                                                                                                      Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
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16-FEB-2001; 2001US-0269308P.
                                                                 21-MAR-2001; 2001WO-US009180
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Xu HH;
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WO200170955-A2
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                                                                                                                                                  23-OCT-2000;
27-NOV-2000;
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Query Match
Best Local Similarity 35.5%
Matches 100; Conservative
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(1) a vector comprising a proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid are included are:

(2) a vector comprising a promoter operably linked to the nucleic acid acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the artisense antisense nucleic acid; (4) an antibody capable of specifically binding compounding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation. Or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound acts; (9) manufacturing an antibiotic; (10) profilling a compound acts; (9) manufacturing an antibiotic; (12) determining the extent or compound that inhibits proliferation of a compound that inhibits proliferation of a compound that inhibits proliferation of a compound that inhibits or collection of a gradien or streaming the conditional acids required confidentifying proteins or screening for homologous nucleic acids required confident acids required confident acids and acids and decompound acids and acids and acids and decompound acids and ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Forsyth RA,
                                                                                                                       Protein encoded by Prokaryotic essential gene #14408
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25, SEQ ID NO 56805; 1766pp; English.
                     ABU28881 standard; protein; 302 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                           06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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                                                                                      (first entry)
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Trawick JD,
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                                                                                                                                                                                         Escherichia coli.
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                                                      ABU28881;
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Wall D,
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the
                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                   GEMVGKKREMQARLEQHKERMAQWASQ--LPKGTRVAPGTSREQOFNLHTQETWTGSVLA
                                                                                                                                                                                                                                                       86 VGTRAQPSLEAIAALKPDLIIADSSRHAGVYIALQQIAPVLLLKSRNETYAENLQSAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 OLGFKEALSDDVTKGLSKYLKGPYL-OMNTETLSQVNPERMFIMTNKASSNEPSLKELEK
                                                                                                           45 IXHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                              26 VQDEHGIFTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS
                                                                                                                                                                                                                       105 VGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
                                                                                                                                                                                                                                                                                                                                      165 SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ဌ
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                          16;
27.2%; Score 460; DB 6; Length 302; 35.5%; Pred. No. 4e-29;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Äξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 DPVWKKLNAVKNQRVDILDRDLWARSRGLISSEBMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #27023.
                                                       62; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 69420; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU41496 standard; protein; 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas syringae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-029926/02.
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                                                                                                                                                                                                                                                                                                                                                                135 YKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITM 194
                                                                                                                                                                                                                                                                                                                                                                                                   DKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                       255 TLSQVNPERMFIMTNK----ASSNEPSLKEL-EKDPVWKKLNAVKNQRVDILDRDLWARS 309
                                                                                                                                                                                                                                                                                                    | ::|:||||||||:|| 5 LLTLIASAA-----QAAPIDIDDGQHKWHLPDTPKRWVLEFSFLDGLAS 49
                                                                                                                                                                                                                                                                                        17 LFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKV--PKHPKRVVVLEYSFVDALVA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                     Length 297;
                                                                                                                                                                                                                                                   26.9%; Score 454; DB 6; Length 29
34.3%; Pred. No. 1.2e-28;
ive 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus protein SEQ ID #5193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW89745 standard; protein; 330 AA.
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272 RGIMASEQIADDALAVLK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 RGLISSEEMAKELVELSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                             Best Local Similarity 34.3
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxic shock syndrome
                                                                                                                                                                                                                                   Sequence 297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW89745;
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
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This sequence represents a Staphylococcus aureus protein sequence of the invention. The DNA sequences encoding the S.aureus proteins are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM). Lead-only memory (ROM) or CD-ROM.

Godisk, random access memory (RAM) aequences allows putative (functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained.

Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a waccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food to in numerous to stee season including cellulitis, eyelld infections, food in numerous to stee shock syndrome, etc. Organisms transformed with the skin syndrome, toxic shock syndrome, etc. Organisms transformed with the skin syndrome, toxic shock syndrome, etc. Organisms transformed with the skin syndrome, toxic shock syndrome, etc. Organisms transformed with the skin syndrome, toxic shock syndrome, etc. Organisms transformed with the skin syndrome are used for recombinant production of the polypeptides.

Che new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the 5191 S.aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGQFLSOLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 FQK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAĞEILNDLGFKR-----NKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.0%; Score 405; DB 2; Length 330; 32.8%; Pred. No. 1.4e-24; ive 65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                Fannon MR,
                                                                                                                                                                                                                Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 3189-3190; 3271pp; English.
                                                                                                                                                                                                                Barash SC,
                                                                                  97EP-00100117
                                                                                                                              96US-0009861P
                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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Matches 113; Conservative
                                                                                                                                                                                                                                                            WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                      S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 330 AA;
                                                                                                                              05-JAN-1996;
                                                                                    07-JAN-1997;
EP786519-A2
                                         30-JUL-1997
                                                                                                                                                                                                                   Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AAY42331 standard; protein; 330

RESULT 24 AAY42331 ID AAY

Staphylococcus aureus,

us-10-724-972a-6352.rag

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241 SKYLKG--PYLOMNT-ETLSOVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLINA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Staphylococcus nucleic acid molecules, used to develop products for the diagnosis, prevention and treatment of Staphylococcal
                           179 FQK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAGEILNDLGFKR-----NKDL
YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the deduced sequence of the novel 36.8 kDa cbrA protein of Staphylococcus aureus strain ISP3 (ATCC 202108), as predicted from
                                                                                                                                                               293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                      289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "antigenic epitope-bearing region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "antigenic epitope-bearing region"
                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus iron regulation protein cbrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233. .236
/note= "antigenic epitope-bearing
243. .247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epitope-bearing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .54
.te= "antigenic e
                                                                                                                                                                                                                                                                                                         AAY31824 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 25; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(LUDW-) LUDWIG INST CANCER RES
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98US-0080296P.
98US-0084674P.
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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309. .31
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-562101/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iron regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1998;
01-APR-1998;
07-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson AJG,
                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-1999
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents Staphylococcus aureus cbrA protein. The cbrA protein is predicted to have a molecular weight of about 36.8 kD and, along with cbrB (AAY42312) and cbrC (AAY42313), is thought to be involved in iron regulation, based on amino acid sequence homology with known iron regulations in burns, callulitie, eyelid infections, food poisoning, joint infections in burns, callulitie, eyelid infections, food poisoning, joint infections, neonatal conjunctivities, osteomyelities, skin infections, infections, acalded skin syndrome and toxic shock syndrome. Surgical wound infection, scalded skin syndrome and toxic shock syndrome. Surgical wound infection, scalded skin syndrome and toxic shock syndrome. Surgical wound infection, scalded skin syndrome and toxic shock syndrome. The chicillin-resistant strains generally being multiply drug resistant. Methicillin-resistant strains generally being multiply drug resistant. Strains being multiresistant against virtually all antiblotics with the exception of the vancomycin-type glycopeptide antiblotics. The protein may be useful to screen potential antagonists which could be used as antiblotics and it may be used as a vaccine to prevent or attenuate an infection caused by a member of the Staphylococcus genus. The protein, or antibodies against it can be used in immunoassays to detect Staphylococcus in a biological sample. Probes and primers derived from the nucleic acid sequences may also be used to detect Staphylococcus mucleic acid sequences may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 KVRNEKVYDQLSKIAPTV---STDTVFKFK-DTTKLMGKALGKEKEAEDLLKKYDDKVAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 IKML-VVTLAFILLV-LAGCSGNSNKQSSDNKDKETTSIKHAMGTTEIKGKPKRVVTLYQG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIXHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%; Score 405; DB 2; Length 330;
32.8%; Pred. No. 1.4e-24;
ive 65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus genes and polypeptides, vectors and methods of
                                                                                                                           Infection; detection; diagnosis; screening; antibiotic; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
                                                                                   Staphylococcus aureus cbrA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 25; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC.
LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                              98US-0078682P.
98US-0080296P.
98US-0084674P.
                                                                                                                                                                                                                                                                                                           99WO-US006199
                                           (first entry)
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Best Local Similarity 32.84
Matches 113, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH;
                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-580304/49.
                                                                                                                                                methicillin, MRSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ22850.
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                                                                                                                                                                                                                           WO9947662-A1.
                                                                                                                                                                                                                                                                                                             L8-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                   20-MAR-1998;
                                         20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                     01-APR-1998;
07-MAY-1998;
                                                                                                                                                                                                                                                                     23-SEP-1999
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      AAY42331;
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           homology to known proteins involved in iron regulation. The invention provides 11 novel genes (see AAZ19882-92) of S. aureus and the provides 11 novel genes (see AAZ19882-92) of S. aureus and the host cells, antibodies and hybridomas. The invention further relates to screening methods for identifying agonists and antiagonists of S. aureus polypeptide activity, and to diagnostic methods for detecting staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. Antagonists of cbrA may be useful as antibiotics to treat infections of S. aureus and other Staphylococcus spp. Also provided are novel vaccines for the prevention or attenuation of infection by Staphylococcus. CbrA polypeptides can also be used to detect S. aureus in immunoassays, as epitope tags, mol.wt. markers, to raise antibodies and as vaccines against S. aureus and other Staphylococcus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SKYLKG--PYLOMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                             FVDALVALDVKPVGIADDNKKONRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                         8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pathogen specific antigen related staphylococcal protein SEQ ID No 346.
                                                                                                                                                                                                                                                                                                                                                                                             YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOFLSOLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
CbrA shows amino acid sequence
                                                                                                                                                                                                                                                                                                  Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                      65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                      24.0%; Score 405; DB 2; 32.8%; Pred. No. 1.4e-24;
genomic DNA (see AAZ19889).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.8
Matches 113; Conservative
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                                                                                                                                                                                                                                                                   Sequence 330 AA;
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma cool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the confirmation of 53-2261 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament or against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoinmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention
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                                                                                                                                                                                                               Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
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C, Henics T,
, Weichhart T,
   Meinke A, Nagy E, Von Ahsen U, Klade C
Minh DB, Vytvytska O, Etz H, Dryla A,
                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 214; 252pp; English.
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                                                                                                                                                   WPI; 2003-075410/07.
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                                                                           Tempelmaier B;
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                                                                                                                                                                                                                                                                                                                                        preparation.
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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ATDVAVSLGVKPVGAVESWTQKPKFYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL-----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP). To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and annino acid domains. The present SEIP has sequence were deduced and analysed for conserved and/or functional domains. The present SEIP has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can antibodies useful in passive or active immunisation strategies to preven or contain staphylococcal infection. They can also be used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNRHKGIYKDLNKI APTIELKSFDGDYNENIDAFKTI SKALGKEBEGKKRLEEHDKKIBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
                                                                                                           Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                Staphylococcal surface-exposed immunogenic polypeptide D2 SA02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.0%; Score 405; DB 6; 32.8%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                  (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 51; 62pp; English
                                                                                                                                                                                                                                                                                                                       17-JUN-2002; 2002WO-US019224.
                                                                                                                                                                                                                                                                                                                                                                    17-JUN-2001; 2001US-0298975P.
                   11-AUG-2003 (first entry)
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                                                                                                                                      antibacterial; vaccine
                                                                                                                                                                                 Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 330 AA;
                                                                                                                                                                                                                              WO2003020875-A2
                                                                                                                                                                                                                                                                            13-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scott DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKQVDNGKDIIQLISKESIPLMNADHIFVVKSDPNAKDAALVKKTESEWISSKEWKNLDA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolating microbial target surface exposed immunogenic polypeptides, by immunizing host with microbial membrane-associated polypeptides to produce antibodies and using antibodies to isolate target polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of target surface exposed immunogenic polypeptides (SEIP) from microorganisms. The SEIP's of the invention are receptors of iron-binding molecules. The activity of polypeptides of the invention may be described as antibacterial, fungicide and protozoacide. Pharmaceutical compositions based on the polypeptides of the invention are useful for treating infections and diseases caused by microbes including bacteria, fungi and protozoa in a patient. They are also useful for topical disinfection in an animal or mammal e.g. human. The current sequence represents an SEIP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVBIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAGBILNDLGFKR-----NKDL
                   SEIP; surface exposed immunogenic polypeptide; iron-binding; recantibacterial; fungicide; protozoacide; infection; disinfection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.0%; Score 405; DB 6; 32.8%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                    (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 40; 46pp; English.
                                                                                                                                                                                                                            10-JUL-2002; 2002WO-US021663.
                                                                                                                                                                                                                                                                         10-JUL-2001; 2001US-0304390P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-221756/21
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Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 330 AA;
                                                                                                                                   WO2003006672-A2
                                                                                                                                                                                 23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                  Scott DL;
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RESULT 28 ABR41864 ID ABR41 XX AC ABR41

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Length 330;

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid, (2) a host cell containing the vector, (3) an isolated cuding a polypeptide whose expression is inhibited by the antisense contained or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding carter polypeptide, (5) producing the polypeptide, (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation required gene product or that has an activity acidentic and some required for cellular proliferation or the biological contains a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the gene computed the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the each of the strains is present in a culture or collection of cto which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antieense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL-----KELEKDPVWKKLNA
                                                                                                                                                                                                                                          293 VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                  289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 45599; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU17675 standard; protein; 324 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02.
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                                          179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a new isolated nucleic acid molecule comprising: a sequence that is 95% identical to a fully defined sequence having 586-226 bp, or its complement; or a sequence encoding a polypeptide having a fully defined sequence comprising 136-691 amino acids, or its complement. The gene is Staphylococcus aureus gene. The nucleic acid is useful for preparing a vaccine against infection caused by Staphylococcus aureus. The methods are useful for preventing or attenuating an infection caused by a Staphylococcus, detecting Staphylococcus nucleic acids in a biological sample obtained from an animal, and detecting Staphylococcus auribudies in a biological sample obtained from an animal. This is the amino acid sequence of Staphylococcus aureus cbrA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus gene, useful for preparing a vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.0%; Score 405; DB 7; Length 330;
Best Local Similarity 32.8%; Pred. No. 1.4e-24;
Matches 113; Conservative 65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; immunostimulant; vaccine; vaccine;
Staphylococcus aureus infection; infection prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection caused by Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 16; 61pp; English.
                                                                                                                                                 ADF43556 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0078862P.
98US-0080296P.
98US-0084674P.
99WO-US006199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2002; 2002US-00830217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection attenuation; cbrA
                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cbrA
                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
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07-MAY-1998;
18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1998;
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                                                                                                                                                                                                                  ADF43556;
                                                                                 RESULT 29
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Zyskind JW; Xu HH;

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proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKQPNLEEISKLK 120
                                                                                                                                                                                                                                                                                                                                PDLIIADNNRHKGIYKDINKIAPTIEL---KSPDGDYNENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                          3 KILSI----FIVVFLFAVGCGQQKEEKKETKADNKNQAITIKHAEGETKLDKFAKKVVVL 58
                                                                                                                                                                                                                                                       9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKD----GVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                           40;
                                                                                                                                                                                           Length 324;
                                                                                                                                                                                                                          59; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELKPKKENKMYKLKGDTWIFG-GPESATSLATQVADV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                             23.1%; Score 391; DB 6; 34.4%; Pred. No. 1.9e-23;
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2000US-00649167
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                                                                                                                                                                                              Query Match
Best Local Similarity 34.4
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS73038
                                                                                                                                                                   Sequence 324 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

creaction (PRX) primers, oligomers, and for chomesome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used

cand in recombinant production of (II). The polynucleotides are also used

considered in the sequence tags for identifying expressed

considered in season and as a food

activity of (II) or to treat disease states involving (II). (II) is

cuseful for generating antibodies against it, detecting or quantitating a

consupplement. (II) and its binding partners are useful in medical imaging

consupplement (II) and its binding partners are useful in medical imaging

consupplement. (II) and its binding partners are useful for treating disorders

considered and polymucleotide sequences have applications in

considerating torstain protein expression or biological activity. The

colypopide and polymucleotide sequences have applications in

colypopide and polymucleotide sequences have applications in

cresponsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

amino acid sequences of the invention. Note: The sequence data for this

consideration of cormat directly from WiPo at

consideration of the printed specification, but was obtained in

consideration of the printed specification, but was obtained in

consideration of products dependences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 VGTRAQPSLEAIAALKPDLIIADSSRHAGVYIALQQIAPVLLLKSRNETYAENLQSAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 IKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 VQDEHGTLTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 VGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 QLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 SLGL-----NVPAAMAGASMPSSPGPLGASCPPRCSIHAITVTSTTPCL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --WTPGSVIRCRPVGVLKMTDEAGEDAKLVAVPHSKLSKEYDHIKDVNDLPELLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 PVWKKLNAVKNORVDIL-----DRDLWARSRGLISSE----EMAKELVELSK 327
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.2%; Score 375; DB 4; Length 1132; 32.5%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52, Mismatches 115, Indels
                                                                                                                     Claim 20; SEQ ID NO 39210; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #13139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG13148 standard; protein; 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 32.5%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
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AAG90121 standard; protein; 315 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                  The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (ftp. wipo.int/pub/published_pot_esseries)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S58 VQDEHGTFTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 VGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%; Score 350; DB 4; Length 932; 46.6%; Pred. No. 1.7e-19; ive 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 43507; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKALGKEEEGKKRLEEHDKKIEEYKKEI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 GEMVGKKREMQARLEQHKERMAQWASQL 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus protein #2290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM73050 standard; protein; 287
                                                                                                                                 Tang YT;
                              30-MAR-2001; 2001WO-US008631
                                                         31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 46.6%
nes 69; Conservative
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                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                            WPI; 2001-639362/73.
N-PSDB; AAS77335.
                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 932 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
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Matches
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50 GTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRK 109

2 GTTEIKGKPKRVVTLYQGATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEP

61

110 OPNIEEISKIKPDIIIADNNRHKGIYKDINKIAPTIELKSFDGDYNENIDAFKTISKALG 169 62 APNLEEISKLKPDLIVASKVRNEKVYDQLSKIAPTV---STDTVFKFK-DTTKLMGKALG 117 KEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOF 222 LSQLGPKEALSDDVTKGLSKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL- 278 ----KELEKDPVWKKINAVKNQRV-DILDRDLWARSRGLISSBEMAKELVELSKKDSKKD 333 KKTESEWTSSKEWKNLDAVKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQ 285

170

223 174 279 228 NK 335 :| SK 287

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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the novel S. aureus proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scarselli M;
enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                      27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97; Conservative
                                                                             Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-120786/11.
N-PSDB; ACF74610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 287 AA;
                                                                                                                                                   WO200294868-A2.
                                                                                                                                                                                                                            28-NOV-2002
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino scids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 KGIYKDLMKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTETLSQVNPERMP--IMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 LVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAIYDQLSDIAPTVMSEGSGTNWNEQAE---ITAAAVNKSDEMDKLISDLDTRATELGEE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQM 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 VIGLLFVLIATAACGNNSSSNS-SKESSKDGVEIKHBEGTTKVPKHPKRVVVLEYSFVDA
                                                                                                                                                                                                                                                                                                                                                                                                                  Ochiai K, Yokoi H;
                                                                           Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17, SEQ ID NO 3875; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 331; DB 4; Length 315; 28.6%; Pred. No. 1.5e-18; ive 65; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                       C glutamicum protein fragment SEQ ID NO: 3875.
                                                                                                                                                                                                                                                                                                               07-APR-2000; 2000JP-00159162.
                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                          18-DEC-2000; 2000EP-00127688
                                                                                                                                       Corynebacterium glutamicum
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.6
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-376931/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 315 AA;
                                                                                                                                                                                                                                                                                               16-DEC-1999;
07-APR-2000;
26-SEP-2001
                                                                                                                                                                            EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa S,
Tateibhi N,
                                                                                                                                                                                                                   20-JUN-2001
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the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits ellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the set compound that inhibits proliferation of the strains is present in a culture or collection of proliferation of an organism; (12) identifying the extent or collection of an organism; (13) identifying the target of a compound that inhibits the proliferation of an organism or (13) identifying the target of a compound calls are useful for dentifying profering or exceeding for homologous nucleic acids required for cellular proliferation of an organism and proliferation of an organism. The antisense nucleic acids are useful for the proliferation of the strains or solvering and proversors and proversors and proversors are cardinal actions and acceptance or solversors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #10870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 53267; 1766pp; English.
                                                                                                                                                ABU25343 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.
|:::|::|
298 IGVLGANEILDDLEE 312
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                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                         Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200277183-A2.
                                                                                                                                                                                                                                             19-JUN-2003
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                                                                                                                                                                                             ABU25343;
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                                                                                                 RESULT 3:
ABU25343
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an isolated nucleic acid comprising any one of

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01-JAN-2004
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                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                 NRHKGIYKDLNKIAPTIELKSFDGDYNE----NIDAFKTISKALGKEEEGKKRLEEHDKK 184
                                                                                                                                                                            124 GRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNID---KIAKIFGVEEKANQEFSKIEKK 180
                                                                                                                                                                                               IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYL 244
                                                                                                                                                                                                                                   245 KGPYLOMNTETLSQVNPERMFIM----TNKASSNEPSLKELEKDPVWKKLNAVKNQRVD 299
                                                                                                                                                                                                                                              235 HGQ--NITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKNDNII 292
                                                                                 70
                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                           181 IETLNKKVT-DKNLNALTIMVNEGNLSVFGEESRFSILYNSFGF----ENKDKNIKESS
                                                                                 11 LSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVD
                                                                                                                     ALVALDVKP - - VGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                30; Gaps
                                             Length 321;
                                             ; Score 327; DB 6; Length 32; Pred. No. 3.2e-18; 55; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #3886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 46283; 1766pp; English
in electronic format directly from WIPO at
        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                        ABU18359 standard; protein; 314 AA
                                                                                                                                                                                                                                                                         300 ILDRDLW-ARSRGLISSEEM 318
                                                                                                                                                                                                                                                                                          293 YLDSPTWYVNDGGLTSLNKM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                             19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB: ACA22229
                            Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2.
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25-OCT-2001;
08-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                           ABU18359;
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                                                                                                                                                                                                185
                                             Query Match
Best Local
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Wall
                                                                Matches
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The involution relates to an inclusion where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a propertied whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense continued and the second is inhibited by the antisense cartiseration; (2) a host cell containing the vector; (3) an isolated continued to polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) centured for cellular proliferation or the biological pathway in which a proliferation for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling to proliferation of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful of creatined for proliferation to isolate condicate molecules for rational cut encounded by one of the target prokaryotic essential genes. New Jessent sequence data for this patent did not form part of the printed specification, but was obtained for proliferation or an encounded by one of the condition of the printed specification, but was obtained for the print sequence and determined for proliferation or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYLKGPYLOMNTETLSOVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNORVDIL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LKOTMAQVSLEGLVAFQPDQMFIV-NFGGEADKVYEDYKNSAVWKDNKAVKONNHVYEV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYV-GOFLSQLGFKEALSDDV----TKGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%; Score 313; DB 6; I
29.9%; Pred. No. 4.3e-17;
tive 65; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRDLW-ARSRGLISS----EEMAKELVELSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNEVFNTKAFNPIGKDMLIDEIAKEILAKNK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. faecium protein sequence SEQ ID 4516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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The invention relates to an isolated nucleic acid derived from Enterococcus faccium encoding an Enterococcus faccium polypeptide having one of 10 fully defined sequences given in the for comprising 40 acquential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridishing to it). Also included are a renomblant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids are called is useful for diagnosing pathological conditions resulting from E. faccium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faectium infections. The present sequence represents the presents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 SKLKPDLIIADNNRHKGIYKDLNKIAPTIBLKSFDG-----DYNENIDAFKTISKALGKE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGKKRLEEHDKKI EEYKKEI TMDKNQKVL PAVAAKSGLLAHPSNSYVGQFLSQLGFKEA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRGLKILSVIGLLFVLIATAACG--NNSSSNSSKESS---KDGVEIKHEEG-TTKVPKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 VVGILILASFGL-----AACGNSNNTSQADTKKSSTQTETTLTITDSNGDQIBVPNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRVVVLEYSFVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 307.5; DB 7; Length 31.3%; Pred. No. 1.4e-16; ive 65; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1, SEQ ID NO 4516; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      one if the disclosed E. faccium proteins.
                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                   98US-00107532.
                                                                                                                                                                                                                    97US-0051571P
                                                                                                                                                                                                                                                                                                                Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 107; Conservative
                                                                        Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                    2003-799836/75.
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                                                                                                                                                                                                                                                                                                                                                                   N-P8DB, ADC91235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
                                                                                                                                                                                   30-JUN-1998;
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14-MAY-1998;
                                                                                                           US6583275-B1
                                                                                                                                               24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection.
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262 --DDQIEASTHGGS------VSYEYVLEKNPDILFVVDRTKAIGGDDSKDDISANEL 310

232 LSDD----VTKGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPV

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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the mucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
of polypeptide acid; (2) a host cell containing the vector; (3) an isolated
collipse acid; (4) an antibody capable of specifically binding
antisense nucleic acid; (4) an antibody capable of specifically binding
collipreration or the activity of a gene in an operon required for
proliferation or the activity of a gene in an operon required for
colliferation or the activity of a gene in an operon required for
colliferation or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
compound's activity, (11) a culture compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
co which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
crains or (13) identifying the target of a compound that inhibits for
conditieration of an organism. The antisense nucleic acids are useful for
dentifying proteins or screening for homologous nucleic acids required
conditieration of secretion to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                         311 VAQTWAGKAQQIISLEPDVWYLSGGGLESMKLMIEDVWQAFK 352
287 WKKINAVKNQRVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #2988.
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                                                                                                                                                          ABU17461 standard; protein; 314
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                       Bacillus anthracis.
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                                                                                                                                                                                                       ABU17461;
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                                                                                                                  RESULT 38
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Matches
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                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                    AAKPDLILV-NNRQEKIYDQLSKIAPTVMLKT---PLDQWRPKFEEVGQIFGKEKETKEW 171
                                                                                                                                                                                                                                    FKOYD-------EKASKIHDKIVAKTGDAKFMKMAAYP-NAF--RVYGDYGYGSV 216
                                                                                                                                                                                                                                                       287
                                                                                                                                                                                                                                                                 -----KKNRIIKPL----RDKIGKYTSVGTRKQPNLEEIS 117
                                                                                                                                                                            KLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                 LEEHDKKIEBYKKEITMDKNQKVLPAVAAKSG-----LLAHPSNSYVGQFLSQLGFKEA 231
                                                                                                   70
                                                                                                                     67
the target prokaryotic essential genes. Note; The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                   16 LLFVLIAT----AACGNNSSSNS-SKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVD
                                                                                                               LSDDV----TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                 16;
                                                               17.8%; Score 301; DB 6; Length 314; 27.3%; Pred. No. 4.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                  66; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                             KKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                             KNMNAVKNNHV------FTIKNEELNKGYFPLGKE 301
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #3796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
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                                                                                                                                                                                                                                                                                                                                                             ABU18269 standard; protein; 264
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2001US-0342923P.
2002US-00072851.
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                                                                                                                                          ALVALDVKPVGIADDN---
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                                                                                  93; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus anthracis
                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACA22139
                                               Sequence 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200277183-A2.
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the invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

(2) a vector comprising a promoter operably linked to the nucleic acid concluded by the antisense antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or that has an activity against a biological pathway in which a proliferation, or that has an activity typical cellular proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits spone product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; a activity; (11) a culture comprising strains in which the cest compound that inhibits proliferation of the strains is activity; (11) a culture comprising strains in which the cest compound that inhibits proliferation of an ordanism. The antisense mucleic acids required for proliferation in cells other candidate molecules for rational correlative form proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent directly from NIPO at contractor, of the princed appecification, but was obtained for proliferation of the princed appecification, but was obtained for proliferation of the princed appecification, but was obtained to the contract of the princed appecification, but was obtained and the contractors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEEHDKKIEEYKKEI----TMDKNOKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ladmokaradakakiekadikokniamaqartakonvetrrili--dnslalovtkkig-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKQPNLEEISKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Mismatches 102; Indels
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SEQ ID NO 46193; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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ABN90518 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37560. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DKKKISNITVEVPKNPKNAVVLDYGALDVL-----KELGVADKVKGLPKGENNQSLPKFLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 EFKDDKYINTGNLKEVNFDKVASAKPDVIFISGRTANQKNLDEFKKAAPKAKV-VYVGTS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 NENI -- DAFK----TISKALGKEREGKKRLEEHDKKIEBYKKEITMDKNQKVLPAVAAKSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 DDNLIKDMKKVYTENLGKIYDKEDKAKKINKDLDRKISDMKDK-TKDFNKKVWYLLVNBGE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 LSTFGPGGRFGGLVFDTLGFKPA------DKKVSKSPHGQNINNEYINKQNPDVILAM 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 DRGSVVGGKATTN-----QVLKNKVIKNVKAVKSNHIYELDPKLMYFSSG--SSTTTIKQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLAH-PSNSYVGOFLSOLGFKEALSDDVTKGLSKYLKGPYLQ-MNTETLSOVNP---- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 ERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KIGKYTSVGTRKQPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKES-SKDGVEIKHE------ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNK-----KNRIIKPLRD 97
                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.5%; Score 296.5; DB 5; Length 351; 28.4%; Pred. No. 1.1e-15; tive 70; Mismatches 131; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 5492; 267pp; English
                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                          97US-0055779P.
                                                                                                                                         98US-00134001
antibacterial; gene therapy
                                                                                                                                                                                                                                                                Doucette-Stamm LA, Bush D;
                                    Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.4*
Matches 104; Conservative
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N-PSDB; ABN93192.
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                                                                      US6380370-B1
                                                                                                                                           .3-AUG-1998;
                                                                                                                                                                           14-AUG-1997;
08-NOV-1997;
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